

//0.99:63:36//CITROBACTER FREUNDII.//069280  
 F-PLACE1007409//WHITE PROTEIN.//7.9e-38:179:41//DROSOPHILA MELANOGASTER  
 (FRUIT FLY).//P10090  
 F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL A  
 CTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-  
 2) (ADABP).//0.031:159:23//HOMO SAPIENS (HUMAN).//P27487  
 F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN KOX27) (FRAG  
 MENT).//0.023:36:50//HOMO SAPIENS (HUMAN).//P17038  
 F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CCP1-MET1 INTERGENIC REG  
 ION.//2.2e-18:85:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36149  
 F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//0.66:13:53//C  
 HLAMYDOMONAS REINHARDTII.//Q06480  
 F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:45:33/  
 /SUS SCROFA (PIG).//Q35914  
 F-PLACE1007478//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR  
 ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//5.3e-08:50:56//MUS MUSCULUS (  
 MOUSE).//P11369  
 F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION  
 .//0.87:43:37//ESCHERICHIA COLI.//P03849  
 F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO  
 /RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//1.2e-25:202:31//HOMO SAPIEN  
 S (HUMAN).//P98174  
 F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TAF60-G4P1 INTERGENIC RE  
 GION.//0.12:128:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53139  
 F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (  
 CK 19).//2.1e-45:209:48//BOS TAURUS (BOVINE).//P08728  
 F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN.//0.74:80:30//VACCINIA VIRUS  
 (STRAIN COPENHAGEN).//P20550  
 F-PLACE1007525

F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.045:92:30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P80144

F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180.//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.5e-16:188:34//CAENORHABDITIS ELEGANS.//P34537

F-PLACE1007557

F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.98:72:33//DAUCUS CAROTA (CARROT).//P06600

F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT).//1.7e-11:88:43//HOMO SAPIENS (HUMAN).//Q03936

F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP).//0.19:109:27//MUS MUSCULUS (MOUSE).//P13808

F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.98:34:41//PSEUDOMONAS AERUGINOSA.//P23621

F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.70:110:34//BOSTAURUS (BOVINE).//P02465

F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:20:45//STRUTHIO CAMELUS (OSTRICH).//021401

F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.1e-06:197:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.0:47:46//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO).//Q26457

F-PLACE1007690//SPERM PROTAMINE P1.//0.12:26:50//TACHYGLOSSUS ACULEATUS



ACULEATUS (AUSTRALIAN ECHIDNA).//P35311  
 F-PLACE1007697//SPERM PROTAMINE P1.//0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305  
 F-PLACE1007705//BIOH PROTEIN.//0.015:97:29//ESCHERICHIA COLI.//P13001  
 F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1).//5.3e-55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32898  
 F-PLACE1007725  
 F-PLACE1007729//PROTEASE (EC 3.4.23.-).//1.8e-21:136:42//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10271  
 F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.0031:77:40//HOMO SAPIENS (HUMAN).//P81489  
 F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.78:39:56//HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE1007743  
 F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT).//0.0066:168:25//HOMO SAPIENS (HUMAN).//Q14690  
 F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT).//0.62:17:41//LITHOBIUS FORFICATUS.//Q01872  
 F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//1.0:40:30//BACILLUS SUBTILIS.//P54446  
 F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A).//0.79:28:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01530  
 F-PLACE1007829//SPORE COAT PROTEIN G.//1.0:65:38//BACILLUS SUBTILIS.//P39801  
 F-PLACE1007843  
 F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-32:37:94//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOH (GTP-BINDING PROTEIN TTF).//8.7e-05:138:30//HOMO SAPIENS (HUMAN).//Q15669

F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN.//0.0039:127:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50275

F-PLACE1007866

F-PLACE1007877

F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTIGEN).//0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60522

F-PLACE1007908//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.5e-28:61:65//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.84:48:37//PSEUDOMONAS AERUGINOSA.//P04139

F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//0.00070:96:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38226

F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.//0.00027:255:23//CAENORHABDITIS ELEGANS.//Q09625

F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17).//1.7e-09:127:30//MUS MUSCULUS (MOUSE).//P70453

F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//2.4e-05:104:37//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-PLACE1007990//SPERM PROTAMINE P1.//0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307

F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//1.2e-16:128:39//RATTUS NORVEGICUS (RAT).//Q63622

F-PLACE1008002

F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107)  
(107 KD NUCLEOPORIN) (P105).//3.9e-106:208:93//RATTUS NORVEGICUS (RAT).  
//P52590

F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.9e-09:49:53/  
/BOS TAURUS (BOVINE).//P25508

F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//0.00025:100:27  
//EGGPLANT MOSAIC VIRUS.//P20126

F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO).//0.90:74:  
25//MYCOBACTERIUM TUBERCULOSIS.//053230

F-PLACE1008111//HYPOTHETICAL PROTEIN MJECS12.//0.30:38:42//METHANOCOCCUS  
JANNASCHII.//Q60311

F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN).//0.0085:117:34//SACCHAROMYC  
ES CEREVISIAE (BAKER'S YEAST).//P40091

F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//1.8  
e-06:154:36//GALLUS GALLUS (CHICKEN).//P02467

F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.  
//1.4e-13:227:36//CAENORHABDITIS ELEGANS.//Q09531

F-PLACE1008177//TRICHOHYALIN.//2.7e-10:230:26//OVIS ARIES (SHEEP).//P227  
93

F-PLACE1008181

F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.  
00044:121:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A.//3.0e-05:82:37//MICROPTERU  
S SALMOIDES (LARGEMOUTH BASS).//P38621

F-PLACE1008209//METALLOTHIONEIN-I (MT-I).//0.95:39:35//CERCOPITHECUS AET  
HIOPS (GREEN MONKEY) (GRIVET).//P02797

F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (  
PROCYCLIN) (PARP).//0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI.//P08469

F-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.2e-23:14  
8:38//PODOSPORA ANSERINA.//Q00808

F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).  
//1.1e-97:222:81//BOS TAURUS (BOVINE).//P53620

F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//5.8e-20:161:37//S  
ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12689

F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.1e-23:124:42//H  
OMO SAPIENS (HUMAN).//P08547

F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.06C IN CHROMOSOME I.//  
0.47:99:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14302

F-PLACE1008329//PUTATIVE Z PROTEIN.//0.73:52:28//OVIS ARIES (SHEEP).//PO  
8105

F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-37:75:81/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.1e-08:70:50//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1008356//FRUIT PROTEIN PKIW1501.//0.0037:148:29//ACTINIDIA CHINEN  
SIS (KIWI) (YANGTAO).//P43393

F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:205:30//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1008369

F-PLACE1008392

F-PLACE1008398//GENE 33 POLYPEPTIDE.//1.5e-102:225:84//RATTUS NORVEGICUS  
(RAT).//P05432

F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.9e-08:186:34//M  
US MUSCULUS (MOUSE).//P05143

F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS AS  
SOCIATED PROTEIN) (TAP).//9.4e-105:207:98//BOS TAURUS (BOVINE).//P41541

F-PLACE1008405

F-PLACE1008424//PROTEIN UL56.//1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 /  
STRAIN HFEM).//P36297 ;

F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN  
II).//4.4e-05:185:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q99323

F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.00054:172:25  
//RATTUS NORVEGICUS (RAT).//Q05175

F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.  
//1.9e-23:226:34//CAENORHABDITIS ELEGANS.//P34681

F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN).//0.97:23:52//BUDGERIG  
AR FLEDGLING DISEASE VIRUS (BFDV).//P13893

F-PLACE1008457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.1e-12:89:47//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN KOX29) (FRAG  
MENT).//0.00017:23:43//HOMO SAPIENS (HUMAN).//P17040

F-PLACE1008488//HYPOTHETICAL PROTEIN UL61.//9.1e-05:204:30//HUMAN CYTOME  
GALOVIRUS (STRAIN AD169).//P16818

F-PLACE1008524//HOMEBOX PROTEIN HLX1 (HOMEBOX PROTEIN HB24).//0.95:74:  
36//HOMO SAPIENS (HUMAN).//Q14774

F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.1e-05:86:45/  
/HOMO SAPIENS (HUMAN).//P39192

F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SMP1-MBA1 INTERGENIC REG  
ION.//3.9e-21:62:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38298

F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME I.//3  
.5e-06:118:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09830

F-PLACE1008568//NEURONATIN.//0.046:34:52//HOMO SAPIENS (HUMAN).//Q16517

F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT).//0.94:30:43//LITHOBIUS FOR  
FICATUS.//Q02030

F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155)  
(155 KD NUCLEOPORIN) (P140).//3.9e-123:224:96//RATTUS NORVEGICUS (RAT).

//P37199

F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//5.0e-05:31  
:67//HOMO SAPIENS (HUMAN).//P20931

F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)./  
/0.87:17:52//ORNITHODOROS MOUBATA (SOFT TICK).//P36235

F-PLACE1008626//METALLOTHIONEIN-I (MT-I).//0.77:33:36//SCYLLA SERRATA (M  
UD CRAB).//P02805

F-PLACE1008627//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR)  
(GIF) (GIFB).//0.14:44:31//HOMO SAPIENS (HUMAN).//P25713

F-PLACE1008629

F-PLACE1008630//PROTAMINE Z3 (SCYLLIORHININE Z3).//0.78:33:36//SCYLIORHI  
NUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK).//P30258

F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (I  
ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RE  
LATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120)./  
/1.7e-30:220:41//HOMO SAPIENS (HUMAN).//Q14624

F-PLACE1008650//PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1.//2.5e-  
10:106:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42384

F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//1.0:36:38  
//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321

F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (E  
C 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT).//4.  
8e-14:47:80//HOMO SAPIENS (HUMAN).//000217

F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REG  
ION.//0.66:105:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834

F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC R  
EGION.//0.10:178:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGI  
ON (ORFD3).//0.60:44:34//ESCHERICHIA COLI.//P33669

F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.0e-69:191:80//MUS MUSCULUS (MOUSE).//035345

F-PLACE1008798//BACTERIOCIN LACTOBIN A.//1.0:34:41//LACTOBACILLUS AMYLOVORUS.//P80696

F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.91:77:36//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1008808//REC1 PROTEIN.//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS).//P14746

F-PLACE1008813

F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC REGION.//1.0:62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38309

F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//1.0:82:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN).//0.65:61:36//SOLANUM TUBEROSUM (POTATO).//P15478

F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-56:180:54//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-PLACE1008902

F-PLACE1008920

F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//0.90:77:33//ESCHERICHIA COLI.//P76242

F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5' REGION (ORF3) (FRAGMENT).//0.14:77:45//GLUCONOBACTER SUBOXYDANS.//005543

F-PLACE1008941//ZINC FINGER PROTEIN 141.//1.1e-17:45:95//HOMO SAPIENS (HUMAN).//Q15928

F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//4.1e-14:136:39//MUS MUSCULUS (MOUSE).//P27790

F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.74:37:48//BOS TAURUS

S (BOVINE).//P20072  
 F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0  
 .39:57:36//BALAENOPTERA MUSCULUS (BLUE WHALE).//P41301  
 F-PLACE1009039  
 F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGI  
 ON (F83).//0.48:32:43//ESCHERICHIA COLI.//P46879  
 F-PLACE1009048  
 F-PLACE1009050  
 F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III.  
 //4.9e-23:244:31//CAENORHABDITIS ELEGANS.//P34552  
 F-PLACE1009090//50S RIBOSOMAL PROTEIN L35.//1.0:27:51//MYCOPLASMA GENITA  
 LIUM.//P47439  
 F-PLACE1009091  
 F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT).//3.6e-15:180:30//HOMO SAPIE  
 NS (HUMAN).//Q92832  
 F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FRAGMENT  
 ).//1.4e-94:228:71//MUS MUSCULUS (MOUSE).//P10077  
 F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN).//1.0:49:34//HIRUDINARIA MANILLEN  
 SIS (BUFFALO LEECH).//P81492  
 F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-05:30:83/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.032:40:52//BOS TAUR  
 US (BOVINE).//P20072  
 F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032.//3.3e-37:214:38//HOMO SAP  
 IENS (HUMAN).//Q15034  
 F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-32:56:76/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE1009155//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-17:101:57  
 //HOMO SAPIENS (HUMAN).//P39194



F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J11).//0.0058:73:42//HUMAN C  
YTOMEGALOVIRUS (STRAIN AD169).//P09711

F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//0.0086:9  
6:30//HOMO SAPIENS (HUMAN).//P49902

F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGIO  
N.//1.0:19:52//ESCHERICHIA COLI.//P76246

F-PLACE1009174//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.1e-17:47:82/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE1009183

F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I.//  
0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09783

F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN FATTY-A  
CYL-COA HYDROLASE) (FRAGMENT).//0.027:53:28//RATTUS NORVEGICUS (RAT).//P  
80250

F-PLACE1009200//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.4e-28:84:71/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE1009230//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.8e-12:50:74/  
/HOMO SAPIENS (HUMAN).//P39189

F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN  
(EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7).//1.0:17:52//SOLANUM T  
UBEROSUM (POTATO).//P48504

F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//6.6e  
-41:177:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110

F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).  
//0.00034:108:33//HOMO SAPIENS (HUMAN).//P26371

F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//5.3e-16:84:50/  
/HOMO SAPIENS (HUMAN).//P78352

F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.9e-82:263:67//H  
OMO SAPIENS (HUMAN).//P08547

F-PLACE1009335//60S RIBOSOMAL PROTEIN L32.//0.95:71:36//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P02433

F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF SPLIT 5).//0.90:42:40//MUS MUSCULUS (MOUSE).//P70120

F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1.//0.013:33:48//HOMO SAPIENS (HUMAN).//P04281

F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//0.0022:135:21//CAENORHABDITIS ELEGANS.//P34492

F-PLACE1009388//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.8e-22:73:65//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.1e-83:223:65//HOMO SAPIENS (HUMAN).//P51523

F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.//0.047:145:29//TRITICUM AESTIVUM (WHEAT).//P08489

F-PLACE1009410//TOXIN C13S1C1 PRECURSOR.//0.22:21:47//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329

F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.5.3) (FRAGMENT).//0.81:61:29//ANTHOCEROS FORMOSAE.//Q31791

F-PLACE1009443//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//9.1e-05:93:32//MUS MUSCULUS (MOUSE).//Q62203

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//6.4e-15:41:97//HOMO SAPIENS (HUMAN).//P42356

F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874

F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-34:101:75//RATTUS NORVEGICUS (RAT).//P54319

F-PLACE1009476//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.086:21:52//HOMO SAPIENS (HUMAN).//P30808

F-PLACE1009477

F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X.//  
1.4e-18:138:39//CAENORHABDITIS ELEGANS.//Q11069

F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF E  
XCHANGE FACTOR).//9.4e-80:155:85//HOMO SAPIENS (HUMAN).//Q99418

F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAN/TC4.//1.0:76:26//GIARDIA  
LAMBLIA (GIARDIA INTESTINALIS).//P38543

F-PLACE1009542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00016:31:77//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34) (SUBUNIT I).//0.88:11  
6:29//STREPTOCOCCUS PNEUMONIAE.//Q59952

F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.00023:37:51//RHODOBACTER C  
APSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P30788

F-PLACE1009595

F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN  
C14B1.4 IN CHROMOSOME III.//2.1e-36:116:49//CAENORHABDITIS ELEGANS.//Q17  
963

F-PLACE1009607//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-43:73:69//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1009613

F-PLACE1009621//TRANSCRIPTION FACTOR BTF3 HOMOLOG 2.//0.91:29:44//HOMO S  
APIENS (HUMAN).//Q13891

F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3e-22:132:47//DROSOP  
HILA MELANOGASTER (FRUIT FLY).//P25159

F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CFXA 3' REGION.//0.30:28:  
57//BACTEROIDES VULGATUS.//P30905

F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN).//0.2  
3:79:31//PSEUDOMONAS AERUGINOSA.//Q04591

F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (BRAIN PROTEIN H19) (M

H19) (FRAGMENT).//3.9e-126:227:96//MUS MUSCULUS (MOUSE).//P28660  
 F-PLACE1009665//IG KAPPA CHAIN V-I REGION (HAU).//0.52:89:35//HOMO SAPIENS (HUMAN).//P01600  
 F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19) (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).//0.16:114:29//PAENIBACILLUS MACERANS (BACILLUS MACERANS).//P31835  
 F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//9.6e-19:156:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876  
 F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35200  
 F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P54120  
 F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H6.12C IN CHROMOSOME I.//8.3e-42:171:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09765  
 F-PLACE1009794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.99:36:33//HORDEUM VULGARE (BARLEY).//P17991  
 F-PLACE1009798//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//2.6e-34:191:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779  
 F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.2e-19:190:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968  
 F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.1).//4.4e-20:171:33//BOS TAURUS (BOVINE).//P07688  
 F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.99:30:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779  
 F-PLACE1009886  
 F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTEIN NSP4] (FRAGMENT).//1.0:33:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13896

F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME  
I.//3.1e-42:205:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10190  
F-PLACE1009921  
F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.70:12  
8:29//TRYPANOSOMA BRUCEI BRUCEI.//P24499  
F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.99  
:111:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P30902  
F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258.//0.063:75:32//METHANOCOCCUS  
JANNASCHII.//Q57706  
F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUNOREACTIVE C-KINASE SUB  
STRATE) (BICKS) (FRAGMENT).//0.33:51:45//BOS TAURUS (BOVINE).//P35722  
F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PRO  
TEIN).//0.022:84:27//MUS MUSCULUS (MOUSE).//P28575  
F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BM  
P-1).//0.00011:35:51//HOMO SAPIENS (HUMAN).//P13497  
F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1.//0.052:185:2  
2//CIONA INTESTINALIS.//Q07068  
F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II  
ELONGATION FACTOR DMS-II) (TFIIS).//0.68:98:28//DROSOPHILA MELANOGASTER  
(FRUIT FLY).//P20232  
F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III./  
/6.6e-06:111:32//CAENORHABDITIS ELEGANS.//Q18262  
F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGI  
ON.//0.0024:72:33//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (AC  
MNPV).//P41479  
F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593.//0.83:24:45//HAEMOPHILUS IN  
FLUENZAE.//P44022  
F-PLACE1010069  
F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.000

27:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331  
 F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT).//0.80:39:30//SCIARA COPROP  
 HILA (FUNGUS GNAT).//Q01790  
 F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//2.7  
 e-48:177:46//HOMO SAPIENS (HUMAN).//P98171  
 F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055).//7.9e-07:55:43//HOMO SAPIENS (HUMAN).//P40818  
 F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.0e-107:232:90//RATTUS NORVEGICUS (RAT).//Q62671  
 F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//1.0:33:45//METHANOCOCCUS JANNASCHII.//Q57649  
 F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-PLACE1010106//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.2e-14:94:41//MUS MUSCULUS (MOUSE).//P11369  
 F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION.//4.0e-28:78:76//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53115  
 F-PLACE1010148//GAR2 PROTEIN.//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891  
 F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574  
 F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F.//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175  
 F-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR

SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//1.4e-07:95:  
 43//GALLUS GALLUS (CHICKEN).//P30352  
 F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36).//0.094  
 :109:29//RATTUS NORVEGICUS (RAT).//P47973  
 F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR.//0.99:42:35//LACTOCOCCUS  
 LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068  
 F-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//6.0e-71:201:62//DROSOPHI  
 LA MELANOGASTER (FRUIT FLY).//P25722  
 F-PLACE1010270  
 F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME I.//4  
 .4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014177  
 F-PLACE1010293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-26:94:64//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE1010310//SYNAPSINS IA AND IB.//5.7e-09:89:37//RATTUS NORVEGICUS (  
 RAT).//P09951  
 F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180.//0.033:145:31//PSEUDORABI  
 ES VIRUS (STRAIN KAPLAN) (PRV).//P33479  
 F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD).//0.60:25:4  
 8//MEGABOMBUS PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE).//P04567  
 F-PLACE1010329//TOXIN S5C10.//1.0:39:33//DENDROASPIS JAMESONI KAIMOSAE (  
 EASTERN JAMESON'S MAMBA).//P01419  
 F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.0049:49:55//  
 HOMO SAPIENS (HUMAN).//P39189  
 F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.4  
 7) (VSG LIPASE) (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C)  
 (GPI-PLC).//0.0034:89:30//TRYPANOSOMA CRUZI.//015886  
 F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3)  
 (EC 1.6.99.3) (COMPLEX I-B17) (CI-B17).//1.0:40:35//SUS SCROFA (PIG).//Q  
 29259

F-PLACE1010383

F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.10:174:22/  
/RATTUS NORVEGICUS (RAT).//P41777

F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III./  
/1.5e-21:170:35//CAENORHABDITIS ELEGANS.//P46555

F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REG  
ION.//1.0:31:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.  
//0.77:97:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874

F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.7  
4:45:37//HOMO SAPIENS (HUMAN).//P22531

F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTA  
INS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMM  
A-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDE  
HYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)].//0.70:  
58:39//VIGNA ACONITIFOLIA (MOTHBEAN).//P32296

F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REG  
ION.//0.17:68:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53227

F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.50:48:29//PORP  
HYRA PURPUREA.//P51255

F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571.//0.29:37:43//HAEMOPHILUS IN  
FLUENZAE.//P44260

F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//3.3e-38:1  
78:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747

F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10 (PEROXIN-14).//4.6e-1  
7:192:31//PICHIA ANGUSTA (YEAST) (HANSENULA POLYMORPHA).//P78723

F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3' REGION.//0.44:32:3  
7//PSEUDOMONAS PUTIDA.//P25753

F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//5.0e-06:102:



42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P  
 EPTIDE P-D] (FRAGMENT).//0.00036:134:32//HOMO SAPIENS (HUMAN).//P10162  
 F-PLACE1010628  
 F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-12:37:81/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE1010630  
 F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT).//0.49:62:30//EUMECES SKILTONI  
 ANUS (WESTERN SKINK).//P28118  
 F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN.//1.0:95:30//DROSOPHILA P  
 SEUDOOBSCURA (FRUIT FLY).//Q24617  
 F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (   
 EC 2.4.1.-) (DUGT).//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY)  
 .//Q09332  
 F-PLACE1010702//ZINC FINGER PROTEIN 195.//1.4e-62:117:62//HOMO SAPIENS (   
 HUMAN).//014628  
 F-PLACE1010714  
 F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//1.1e-64:176:76//XEN  
 OPUS LAEVIS (AFRICAN CLAWED FROG).//P50532  
 F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGME  
 NT).//0.97:31:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV  
 -1).//P04612  
 F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//3.8e-05:253:30//M  
 US MUSCULUS (MOUSE).//P05143  
 F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//  
 1.5e-14:175:25//CAENORHABDITIS ELEGANS.//Q09217  
 F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.3e-120:216:8  
 9//MUS MUSCULUS (MOUSE).//Q02614  
 F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN).//0.97:133:24//DROSOPHILA ME

LANOGASTER (FRUIT FLY).//P54623  
 F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC).//0.0060:111:31//ESCHERICHIA COLI.//Q99390  
 F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI.//0.82:44:29//BACILLUS SP. (STRAIN TB-90).//Q07415  
 F-PLACE1010811//CYTOCHROME C-551 (C551).//0.99:42:38//ECTOTHIORHODOSPIRA HALOCHLORIS.//P38587  
 F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN).//2.8e-09:90:34//HOMO SAPIENS (HUMAN).//P41208  
 F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS C LARKII (RED SWAMP CRAYFISH).//P55848  
 F-PLACE1010857//IG ALPHA-1 CHAIN C REGION.//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GORILLA).//P20758  
 F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.2e-56:173:58//HOMO SAPIENS (HUMAN).//Q05481  
 F-PLACE1010877//HEAT SHOCK PROTEIN 82.//0.13:130:25//ZEA MAYS (MAIZE).//Q08277  
 F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//0.95:51:27//BACILLUS SUBTILIS.//P54436  
 F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.-).//0.98:71:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36002  
 F-PLACE1010900//HYPOTHETICAL PROTEIN HI0840.//1.0:42:30//HAEMOPHILUS INFLUENZAE.//P44897  
 F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB3.//0.060:59:35//OVIS ARIES (SHEEP).//P02444  
 F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).//0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9).//P25191  
 F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN.//1.0:17:58//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19285

F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.011:51:45  
 //HOMO SAPIENS (HUMAN).//Q92558

F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15  
 (PROTEIN EPS15).//3.1e-09:64:37//MUS MUSCULUS (MOUSE).//P42567

F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//0.17  
 :71:38//BOS TAURUS (BOVINE).//P41987

F-PLACE1010947

F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//0.011:144:26/  
 /HOMO SAPIENS (HUMAN).//P09493

F-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//1.1e-60:136:52//DROSOPHILA MELA  
 NOGASTER (FRUIT FLY).//P45890

F-PLACE1010965

F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT).//1.0:64:31//DROSOPHILA  
 ANANASSAE (FRUIT FLY).//Q03293

F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H  
 ) (RNASE H).//1.0:32:37//SALMONELLA TYPHIMURIUM.//P23329

F-PLACE1011041//HOMEBOX PROTEIN VAB-7.//0.36:65:30//CAENORHABDITIS ELEG  
 ANS.//Q93899

F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS  
 E BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PL  
 C-154).//1.3e-22:58:93//RATTUS NORVEGICUS (RAT).//P10687

F-PLACE1011054//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-07:38:73/  
 /HOMO SAPIENS (HUMAN).//P39195

F-PLACE1011056//HISTONE H1.//2.2e-10:109:41//PISUM SATIVUM (GARDEN PEA).  
 //P08283

F-PLACE1011057

F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FL05 INTERGENIC REG  
 ION.//1.8e-07:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892

F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5

.4e-25:63:88//RATTUS NORVEGICUS (RAT).//Q07803  
 F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C.//8.4e-31:1  
 57:45//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09916  
 F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-  
 GLYCOPROTEIN).//0.92:58:31//HOMO SAPIENS (HUMAN).//P02743  
 F-PLACE1011143//PROBABLE E5 PROTEIN.//0.24:42:35//HUMAN PAPILLOMAVIRUS T  
 YPE 31.//P17385  
 F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.  
 88:98:27//GLYCINE MAX (SOYBEAN).//Q02917  
 F-PLACE1011165//HISTIDINE-RICH PROTEIN.//0.013:13:76//PLASMODIUM FALCIPA  
 RUM (ISOLATE FCM17 / SENEGAL).//P14586  
 F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.4e-13:98:50//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE1011203  
 F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:48:27//  
 EQUUS ASINUS (DONKEY).//P92479  
 F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//1.9e-15:162:31//S  
 TREPTOMYCES ANTIBIOTICUS.//Q03326  
 F-PLACE1011221//ANTITHROMBIN-III HOMOLOG.//0.84:74:33//FOWLPOX VIRUS (IS  
 Olate HP-438[MUNICH]).//P14369  
 F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (U  
 BIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DE  
 UBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//3.5e-86:  
 218:68//HOMO SAPIENS (HUMAN).//Q13107  
 F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHR  
 OID) (FRAGMENT).//3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485  
 F-PLACE1011273  
 F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0  
 .011:36:50//RATTUS NORVEGICUS (RAT).//P20468

F-PLACE1011296//HOMEBOX PROTEIN DLX-6.//0.76:55:32//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q98877

F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//0.46:43:44//PETUNIA SP. (PETUNIA).//Q07060

F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME I./0.00021:171:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10411

F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR.//7.3e-27:113:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q05211

F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-07:40:62//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//2.2e-54:227:44//MUS MUSCULUS (MOUSE).//Q61703

F-PLACE1011375//PROBABLE E5 PROTEIN.//0.93:28:57//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553

F-PLACE1011399//HISTONE H2B-IV.//0.19:129:27//VOLVOX CARTERI.//P16868

F-PLACE1011419

F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT).//3.4e-05:133:24//GALLUS GALLUS (CHICKEN).//P55879

F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-25:76:63//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN).//0.97:36:41//HOMO SAPIENS (HUMAN).//Q92838

F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1).//0.084:55:30//HOMARUS AMERICANUS (AMERICAN LOBSTER).//P29499

F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1).//0.028:129:34//CLOSTRIDIUM THERMOCELLUM.//Q06852

F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER).//P52178

F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC  
REGION (086).//0.66:32:40//ESCHERICHIA COLI.//P52102

F-PLACE1011520

F-PLACE1011563//LORICRIN.//0.00023:112:39//HOMO SAPIENS (HUMAN).//P23490

F-PLACE1011567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.2e-31:78:76/  
/HOMO SAPIENS (HUMAN).//P39195

F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
)//1.5e-32:45:86//HOMO SAPIENS (HUMAN).//Q05481

F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN  
-SENSITIVE N- TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).//0.26:81:37/  
/HOMO SAPIENS (HUMAN).//Q00975

F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180.//0.00045:170:30//PSEUDORA  
BIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-PLACE1011641

F-PLACE1011643//CUTICLE COLLAGEN 40.//1.0:128:32//CAENORHABDITIS ELEGANS  
.//P34804

F-PLACE1011646//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-15:44:63//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1011649//HYPOTHETICAL PROTEIN F-215.//0.48:106:34//HUMAN ADENOVIR  
US TYPE 2.//P03291

F-PLACE1011650

F-PLACE1011664//CROOKED NECK PROTEIN.//1.2e-79:201:68//DROSOPHILA MELANO  
GASTER (FRUIT FLY).//P17886

F-PLACE1011675//FERREDOXIN.//1.0:44:29//METHANOCOCCUS THERMOLITHOTROPHIC  
US.//P21305

F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC RE  
GION.//1.0:40:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53098

F-PLACE1011719//NEUROTOXIN TX2-6.//0.90:31:35//PHONEUTRIA NIGRIVENTER (B  
RAZILIAN ARMED SPIDER).//P29425

F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//0.0065:125:25//RATTUS NORVEGICUS (RAT).//Q63083

F-PLACE1011729//SRV-RELATED PROTEIN LG27 (FRAGMENT).//0.97:48:39//EUBLEPHARIS MACULARIUS.//P40654

F-PLACE1011749

F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).//0.028:91:39//MUS MUSCULUS (MOUSE).//Q60925

F-PLACE1011778

F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).//0.97:48:43//MUS MUSCULUS (MOUSE).//P20863

F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0027:154:33//BOS TAURUS (BOVINE).//P23206

F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP).//1.0:60:26//PROSTHECOCHLORIS AESTUARII.//P11741

F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION.//0.99:34:35//BACTERIOPHAGE T4.//P39495

F-PLACE1011891//SMOOTHELIN.//0.018:122:31//HOMO SAPIENS (HUMAN).//P53814

F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//6.3e-09:203:35//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-PLACE1011922//CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).//0.067:37:48//MUS MUSCULUS (MOUSE).//P50715

F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE).//1.5e-83:175:89//MUS MUSCULUS (MOUSE).//P53351

F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.50:46:41//SCHEIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//Q02593

F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-05:47:51//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).//0.98:83:31//PLASMODIUM FRAGILE.//P22622

F-PLACE1011995

F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254.//0.032:62:33//HOMO SAPIENS (HUMAN).//Q92543

F-PLACE2000003//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.4e-18:63:73//HOMO SAPIENS (HUMAN).//P39193

F-PLACE2000006//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.14:20:50//BOS TAURUS (BOVINE).//P20072

F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0045:176:30//MUS MUSCULUS (MOUSE).//P05143

F-PLACE2000011//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-25:57:78//HOMO SAPIENS (HUMAN).//P39194

F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.00013:237:27//CAENORHABDITIS ELEGANS.//Q09475

F-PLACE2000015//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-33:60:80//HOMO SAPIENS (HUMAN).//P39193

F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP).//1.0:83:31//HOMO SAPIENS (HUMAN).//P14207

F-PLACE2000021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8).//0.99:103:26//GALLUS GALLUS (CHICKEN).//Q07496

F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.69:29:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642

F-PLACE2000033//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//1.1e-05:74:41//STREPTOMYCES ANTIBIOTICUS.//Q03326

F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).//6.7e-18:191:35//HOMO SAPIENS (HUMAN).//Q02246

F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//4.7e-80:163:96//RATTUS NORVEGICUS (RAT).//P38650



F-PLACE2000047//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//6.4e-06:63:49  
 //HOMO SAPIENS (HUMAN).//P39191

F-PLACE2000050//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.2e-22:74:64/  
 /HOMO SAPIENS (HUMAN).//P39192

F-PLACE2000061

F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS P  
 ROTEIN B).//1.9e-06:108:37//BACILLUS SUBTILIS.//P26907

F-PLACE2000072//ZINC FINGER PROTEIN 165.//3.5e-34:175:49//HOMO SAPIENS (  
 HUMAN).//P49910

F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A  
 ).//0.36:39:38//ONDATRA ZIBETHICUS (MUSKRAT).//P00681

F-PLACE2000100

F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS).//0.18:32:37//ZEA MAYS  
 (MAIZE).//P33626

F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR.//0.056:107:27//HOMO SAPIENS (H  
 UMAN).//Q08708

F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (  
 FRAGMENT).//1.0:21:52//CLOSTRIDIUM PERFRINGENS.//Q46185

F-PLACE2000124//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.4e-37:108:68  
 //HOMO SAPIENS (HUMAN).//P39194

F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85.//0.99:133:29//EPSTEIN-BA  
 RR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03224

F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (  
 VIP-R-2) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RE  
 CEPTOR) (PACAP TYPE III RECEPTOR) (PACAP-R-3).//0.83:65:32//MUS MUSCULUS  
 (MOUSE).//P41588

F-PLACE2000140

F-PLACE2000164//TIPD PROTEIN.//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM  
 (SLIME MOLD).//O15736

F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 PRECURSOR (CARNOBACTERI  
OCIN B1).//1.0:30:26//CARNOBACTERIUM PISCICOLA.//P38579

F-PLACE2000172

F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526.//0.76:44:43//ARCHAEOGLOBUS  
FULGIDUS.//029724

F-PLACE2000187//EM-LIKE PROTEIN GEA6.//0.84:42:35//ARABIDOPSIS THALIANA  
(MOUSE-EAR CRESS).//Q02973

F-PLACE2000216

F-PLACE2000223//NEUROTOXIN III (LQQ III).//0.99:38:34//LEIURUS QUINQUEST  
RIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01487

F-PLACE2000235

F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//5.1e-37:121:42//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE2000264//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//2.4e-05:77:42  
//HOMO SAPIENS (HUMAN).//P39191

F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//5.3e-46:232:45//TRIPNEUSTES  
GRATILLA (HAWAIIAN SEA URCHIN).//P23098

F-PLACE2000302//TRICHOHYALIN.//1.5e-06:215:29//ORYCTOLAGUS CUNICULUS (RA  
BBIT).//P37709

F-PLACE2000305//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.3e-06:33:66//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000317//TOXIN C13S1C1 PRECURSOR.//0.44:45:33//DENDROASPIS ANGUST  
ICEPS (EASTERN GREEN MAMBA).//P18329

F-PLACE2000335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.9e-08:35:71/  
/HOMO SAPIENS (HUMAN).//P39195

F-PLACE2000341//SODIUM/GLUCOSE COTRANSPORTER 1 (NA+)/GLUCOSE COTRANSPO  
TER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.014:141:24//ORYC  
TOLAGUS CUNICULUS (RABBIT).//P11170

F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGI

ON.//5.7e-09:96:38//AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (A  
CMNPV).//P41479

F-PLACE2000347//ZINC FINGER PROTEIN 177.//5.9e-05:49:53//HOMO SAPIENS (H  
UMAN).//Q13360

F-PLACE2000359//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.5e-10:69:52/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE2000366

F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN  
).//1.5e-05:216:29//HOMO SAPIENS (HUMAN).//P54259

F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MN  
T).//0.27:63:33//HOMO SAPIENS (HUMAN).//Q99583

F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN.//0.72:120:31//EQUINE HERPES  
VIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28978

F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.95:40:42//HOMO  
SAPIENS (HUMAN).//P02811

F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-).//0.88:88:31//AEROM  
ONAS HYDROPHILA.//Q07465

F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (C  
D99) (MIC2 PROTEIN) (12E7).//7.6e-16:180:39//HOMO SAPIENS (HUMAN).//P142  
09

F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T  
RNA LIGASE) (LEURS).//1.7e-94:243:64//CAENORHABDITIS ELEGANS.//Q09996

F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP  
5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.2e-09:78:39//MUS MUSCULU  
S (MOUSE).//Q60676

F-PLACE2000419//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-20:61:62//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGENIC REG  
ION.//0.98:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53211

F-PLACE2000427//INSULIN PRECURSOR.//0.98:55:34//CERCOPITHECUS AETHIOPS ( GREEN MONKEY) (GRIVET).//P30407

F-PLACE2000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.5e-07:65:50// HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000435

F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III./ /4.7e-66:178:47//CAENORHABDITIS ELEGANS.//P34678

F-PLACE2000450//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.1e-23:88:62/ /HOMO SAPIENS (HUMAN).//P39195

F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGMENT).//0.093:18:44//CEN TRUROIDES LIMPIDUS LIMPIDUS (MEXICAN SCORPION).//P45630

F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN ).//3.1e-23:165:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450

F-PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.6e-23:73:63// HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-37:90:78/ /HOMO SAPIENS (HUMAN).//P39194

F-PLACE3000004//EYES ABSENT HOMOLOG 3.//1.1e-09:27:100//MUS MUSCULUS (MO USE).//P97480

F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6.//0.0061:148:34//CAENO RHABDITIS ELEGANS.//Q09457

F-PLACE3000020//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (TYPE III ) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//8.8e-93:193:92//RATTUS NORVEGICUS (RAT).//P21932

F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E.//0.15:50:38//METHANOCOCCUS J ANNASCHII.//P54009

F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A.//0.96:50:34//BOS TAURUS (BOV INE).//P48427

F-PLACE3000070//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3' REGION.//0.29:22:

59//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898  
 F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE).//0.99:53:32//BACTERIOPH  
 AGE ALPHA-3.//P31280  
 F-PLACE3000119//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.4e-41:87:78/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.0e-07:269:22  
 //SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22224  
 F-PLACE3000124//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.2e-29:97:73//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1).//0.77:26  
 :42//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P80059  
 F-PLACE3000142//HYPOTHETICAL 7.1 KD PROTEIN IN NAD2 3' REGION (ORF 63).//  
 0.82:34:41//MARCHANTIA POLYMORPHA (LIVERWORT).//P38468  
 F-PLACE3000145//TENSIN.//3.5e-91:238:74//GALLUS GALLUS (CHICKEN).//Q0420  
 5  
 F-PLACE3000147//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-30:61:65/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVER  
 SE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.4e-18:226:34//GIBBON A  
 PE LEUKEMIA VIRUS.//P21414  
 F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.00014  
 :107:33//ZEA MAYS (MAIZE).//P14918  
 F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVER  
 SE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//2.7e-19:169:30//BABOON E  
 NDOGENOUS VIRUS (STRAIN M7).//P10272  
 F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC 2.7  
 .1.-).//0.0061:92:30//MYCOBACTERIUM TUBERCULOSIS.//Q11053  
 F-PLACE3000158//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.7e-49:56:80/  
 /HOMO SAPIENS (HUMAN).//P39189

F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR) (PROTEIN SXY).//0.39:94:34//HAEMOPHILUS INFLUENZAE.//P43779

F-PLACE3000169//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.6e-28:99:59//HOMO SAPIENS (HUMAN).//P39193

F-PLACE3000194//PROLINE-RICH PROTEIN LAS17.//0.91:80:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12446

F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//0.24:119:32//GALLUS GALLUS (CHICKEN).//P16053

F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE3000207//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.5e-09:32:78//HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000208

F-PLACE3000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.2e-34:96:70//HOMO SAPIENS (HUMAN).//P39194

F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING PROTEIN) (BONE GLA- PROTEIN) (BGP).//0.46:13:53//CANIS FAMILIARIS (DOG).//P81455

F-PLACE3000221//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.8e-24:178:45//HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000226//30S RIBOSOMAL PROTEIN S18.//0.98:38:34//NEISSERIA GONORRHOEAE.//007815

F-PLACE3000230//METALLOTHIONEIN (MT).//0.97:25:48//OREOCHROMIS MOSSAMBICUS (MOZAMBIQUE TILAPIA) (TILAPIA MOSSAMBICA).//P52726

F-PLACE3000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).//8.0e-21:121:39//HOMO SAPIENS (HUMAN).//P43361

F-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//2.3e-125:264:87//MUS MUSCULUS (MOUSE).//P53995

F-PLACE3000254//RTOA PROTEIN (RATIO-A).//0.99:142:23//DICTYOSTELIUM DISC

OIDEUM (SLIME MOLD).//P54681  
 F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-12:63:53//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE3000276//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLL  
 AGEN).//1.0:55:38//HOMO SAPIENS (HUMAN).//P27658  
 F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
 .//0.0028:31:54//HOMO SAPIENS (HUMAN).//P30808  
 F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN  
 ).//0.98:82:34//RATTUS NORVEGICUS (RAT).//P54258  
 F-PLACE3000320  
 F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//  
 2.2e-22:61:52//ORYZA SATIVA (RICE).//P25074  
 F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.  
 32:15:53//HOMO SAPIENS (HUMAN).//P22532  
 F-PLACE3000339//CHORION PROTEIN S19.//0.34:89:37//DROSOPHILA VIRILIS (FR  
 UIT FLY).//P24516  
 F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRA  
 GMENT).//1.0:47:38//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P24968  
 F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULO (EC 2.7.1.-).//3.9e  
 -50:168:60//CAENORHABDITIS ELEGANS.//P46549  
 F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.8e-29:76:71/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE3000353//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.  
 41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTI  
 DE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//3.0e-09:100:41//HO  
 MO SAPIENS (HUMAN).//Q10472  
 F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064.//1.0:75:26//TREPONEMA PALLI  
 DUM.//083103  
 F-PLACE3000363//METALLOTHIONEIN (MT).//0.067:42:33//ASTACUS FLUVIATILIS

(BROAD-FINGERED CRAYFISH) (ASTACUS ASTACUS).//P55951  
 F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:65:27//BACTERIOPHA  
 GE PHI-K.//Q38040  
 F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.5e-18:90:47//HOMO  
 SAPIENS (HUMAN).//P10267  
 F-PLACE3000388  
 F-PLACE3000399//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.3e-45:60:75/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-PLACE3000400  
 F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.6e-09:46:73//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.036:43:44//HO  
 MO SAPIENS (HUMAN).//P39188  
 F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE.//0.70:25:40//BOS TAURUS (BO  
 VINE).//P01154  
 F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-09:49:67/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87F.//0.12:42:40//DROSOPH  
 ILA MELANOGASTER (FRUIT FLY).//P08175  
 F-PLACE3000416//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.67:236:21//B  
 OS TAURUS (BOVINE).//P35662  
 F-PLACE3000425//PROLINE-RICH PEPTIDE P-B.//0.45:19:42//HOMO SAPIENS (HUM  
 AN).//P02814  
 F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR.//0.0073:81:43//BOS TAURUS  
 (BOVINE).//P02817  
 F-PLACE3000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE.//1.0:53:32//TACHYPLEU  
 S TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P81281  
 F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7).//0.13:55:32//DENDROASPIS ANGU  
 STICEPS (EASTERN GREEN MAMBA).//P80970



F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//7.0e-19:180:27//HOMO SAPIENS (HUMAN).//P35749

F-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.2e-15:193:30//HOMO SAPIENS (HUMAN).//P46100

F-PLACE4000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR.//0.0024:97:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P22815

F-PLACE4000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-32:79:75//HOMO SAPIENS (HUMAN).//P39194

F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1.//2.2e-99:178:97//MUS MUSCULUS (MOUSE).//P41233

F-PLACE4000063//IMMEDIATE-EARLY PROTEIN.//0.0017:159:25//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01042

F-PLACE4000089

F-PLACE4000093

F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-14:68:60//HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000106//1A PROTEIN [CONTAINS: HELICASE; METHYLTRANSFERASE].//1.0:46:41//BROAD BEAN MOTTLE VIRUS.//Q00020

F-PLACE4000128//HYPOTHETICAL PROTEIN E-115.//0.00020:101:30//HUMAN ADENOVIRUS TYPE 2.//P03290

F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN).//0.15:57:31//HOMO SAPIENS (HUMAN).//P22528

F-PLACE4000131

F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR.//1.0:45:24//BACILLUS SUBTILIS.//P45453

F-PLACE4000156//ZINC FINGER PROTEIN 136.//2.1e-88:194:59//HOMO SAPIENS (HUMAN).//P52737

F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.083:148:26//HOMO SAPIENS (HUMAN).//P52746

F-PLACE4000211//CALPHOTIN.//0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02910

F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-05:20:85//HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE (EC 2.1.1.45) (DHFR-TS).//1.0:96:28//TRYPANOSOMA BRUCEI BRUCEI.//Q27783

F-PLACE4000233

F-PLACE4000247//METALLOTHIONEIN (MT).//1.0e-05:34:41//PLEURONECTES PLATESSA (PLAICE).//P07216

F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//0.99:33:42//CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV).//P31834

F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.42:24:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//3.5e-09:189:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32639

F-PLACE4000261//PEREGRIN (BR140 PROTEIN).//5.0e-11:103:37//HOMO SAPIENS (HUMAN).//P55201

F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.037:181:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//1.0:46:39//MUS MUSCULUS (MOUSE).//P70375

F-PLACE4000300//50S RIBOSOMAL PROTEIN L32.//0.81:28:46//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P80339

F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN).//1.6e-29:44:93//HOMO SAPIENS (HUMAN).//P42345

F-PLACE4000323

F-PLACE4000326//PARATHYMOSIN.//0.0018:54:48//HOMO SAPIENS (HUMAN).//P20962

F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT).//0.97:28:42//S  
US SCROFA (PIG).//Q00968

F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI).//1.0  
:33:36//STOICHACTIS HELIANTHUS (CARRIBEAN SEA ANEMONE) (STICHODACTYLA HE  
LIANTHUS).//P19651

F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.071:4  
2:42//SORGHUM VULGARE (SORGHUM).//P24152

F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-16:54:77/  
/HOMO SAPIENS (HUMAN).//P39193

F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//  
0.25:21:52//HORDEUM VULGARE (BARLEY), AND SECALE CEREALE (RYE).//P25877

F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HE  
ME SYNTHETASE) (FRAGMENT).//0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS.//QO  
5338

F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-29:96:67/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-18:41:73//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//5.4e-21:2  
37:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32639

F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SDL1 5' REGION PRECURSOR.  
//0.00081:210:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40442

F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPT  
ION FACTOR HBP1).//0.020:87:33//TRITICUM AESTIVUM (WHEAT).//P23922

F-PLACE4000465//METALLOTHIONEIN-IL (MT-1L) (MT1X).//0.20:18:38//HOMO SAP  
IENS (HUMAN).//P80297

F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-19:73:52//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000489

F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//0.17:130:30//MUS MUSCULUS (MOUSE).//Q03173

F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT).//3.0e-05:50:36//MUS MUSCULUS (MOUSE).//P10400

F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.//1.8e-45:231:47//RATTUS NORVEGICUS (RAT).//Q07008

F-PLACE4000548//CYTOCHROME C-551 (C551).//0.96:50:34//ECTOTHIORHODOSPIRA HALOPHILA.//P00122

F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55824

F-PLACE4000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//9.7e-11:166:28//HOMO SAPIENS (HUMAN).//P16109

F-PLACE4000590//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.6e-17:134:35//GIBBON APE LEUKEMIA VIRUS.//P21414

F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).//1.0:54:29//RATTUS NORVEGICUS (RAT).//P30969

F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30].//2.6e-14:221:32//MOLONEY MURINE SARCOMA VIRUS (STRAIN TS110).//P32594

F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC REGION.//0.65:37:40//ESCHERICHIA COLI.//P37910

F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT).//1.0:33:33//HOMO SAPIENS (HUMAN).//P17020

F-PLACE4000654

F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION.//1.6e-07:161:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33313  
F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//7.4e-15:223:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//060100

F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//0.0013:128:35//GALLUS GALLUS (CHICKEN).//Q98937

F-SKNMC1000046//CUTICLE COLLAGEN 1.//0.0010:154:33//CAENORHABDITIS ELEGANS.//P08124

F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.2e-41:87:98//HOMO SAPIENS (HUMAN).//P17655

F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR ERBB KINASES).//0.0032:154:35//HOMO SAPIENS (HUMAN).//O14511

F-THYRO1000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//1.6e-23:124:37//CAENORHABDITIS ELEGANS.//Q20939

F-THYRO1000026//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.0e-13:54:66//HOMO SAPIENS (HUMAN).//P39192

F-THYRO1000034//HYPOTHETICAL 10.4 KD PROTEIN.//0.16:44:34//HEPATITIS B VIRUS (SUBTYPE AYW).//P03163

F-THYRO1000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52) (CAMBRIDGE PATHOLOGY 1 ANTIGEN).//0.83:59:37//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P32763

F-THYRO1000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT).//0.25:23:39//BOS TAURUS (BOVINE).//P79244

F-THYRO1000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//2.3e-11:133:36//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-THYRO1000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM.//1.5e-14:205:29//HOMO SAPIENS (HUMAN).//Q00872

F-THYRO1000085

F-THYRO1000092//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.063:  
59:33//HOMO SAPIENS (HUMAN).//P49901

F-THYRO1000107

F-THYRO1000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-58:110:67//N  
YCTICEBUS COUCANG (SLOW LORIS).//P08548

F-THYRO1000121//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//2.  
6e-06:134:35//MUS MUSCULUS (MOUSE).//Q62203

F-THYRO1000124//TENECIN 3 PRECURSOR.//0.047:76:35//TENEbrio MOLITOR (YEL  
LOW MEALWORM).//Q27270

F-THYRO1000129//FIBROSIN (FRAGMENT).//0.35:43:34//MUS MUSCULUS (MOUSE)./  
/Q60791

F-THYRO1000132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.7e-14:104:42/  
/HOMO SAPIENS (HUMAN).//P39188

F-THYRO1000156

F-THYRO1000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.7e-20:71:71/  
/HOMO SAPIENS (HUMAN).//P39189

F-THYRO1000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOC  
IATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNI  
T) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)./  
/6.7e-88:216:76//MUS MUSCULUS (MOUSE).//P35585

F-THYRO1000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.9e-24:72:77/  
/HOMO SAPIENS (HUMAN).//P39192

F-THYRO1000187

F-THYRO1000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT.//0.060:5  
0:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52871

F-THYRO1000197

F-THYRO1000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME III./  
/2.0e-06:88:35//CAENORHABDITIS ELEGANS.//P34379

F-THYRO1000206

F-THYRO1000221

F-THYRO1000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//1.0:51:35//AUTOGRAPHICA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41661

F-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.4e-37:137:36//HOMO SAPIENS (HUMAN).//P51523

F-THYRO1000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.11:21:52//HOMO SAPIENS (HUMAN).//P30808

F-THYRO1000270//WDNM1 PROTEIN PRECURSOR.//0.40:52:32//MUS MUSCULUS (MOUSE).//Q62477

F-THYRO1000279//BETA CRYSTALLIN A4.//0.97:64:26//BOS TAURUS (BOVINE).//P11842

F-THYRO1000288//POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN-SPECIFIC ENDOPROTEASE 1) (PPSEP 1).//3.4e-48:142:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10071

F-THYRO1000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT).//0.87:35:45//MUS MUSCULUS (MOUSE).//P10755

F-THYRO1000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME I.//0.00010:75:26//CAENORHABDITIS ELEGANS.//P90859

F-THYRO1000343//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14].//0.88:107:26//MUS MUSCULUS (MOUSE).//P26339

F-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//4.6e-25:49:81//MUS MUSCULUS (MOUSE).//P17563

F-THYRO1000368//LOCOMOTION-RELATED PROTEIN HIKARU GENKI PRECURSOR.//1.0:136:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09101

F-THYRO1000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN SARCOMA VIRUS.//P03330

F-THYRO1000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.90:46:30/  
 /HALICHOERUS GRYPUS (GRAY SEAL).//P38592  
 F-THYRO1000394//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0  
 0019:48:37//HOMO SAPIENS (HUMAN).//P22531  
 F-THYRO1000395//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-33:186:38//DRO  
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-THYRO1000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT).//0.57:67:31//ST  
 APHYLOCOCCUS AUREUS.//P48860  
 F-THYRO1000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:38//  
 STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997  
 F-THYRO1000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOLIN 61)  
 .//0.31:34:44//CARNOBACTERIUM PISCICOLA.//P38578  
 F-THYRO1000471//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.1e-31:94:72/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1000484//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.9e-08:30:86/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-THYRO1000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.  
 93:98:27//GLYCINE MAX (SOYBEAN).//Q02917  
 F-THYRO1000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//2.4e  
 -51:198:50//MUS MUSCULUS (MOUSE).//P15533  
 F-THYRO1000502//HUNCHBACK PROTEIN (FRAGMENT).//0.84:41:43//APIS MELLIFER  
 A (HONEYBEE).//P31504  
 F-THYRO1000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:231:33//EPSTEIN-BARR V  
 IRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-THYRO1000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).//0.47:58:  
 37//GALLUS GALLUS (CHICKEN).//Q03352  
 F-THYRO1000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00048:64:42//R  
 ATTUS NORVEGICUS (RAT).//P02454  
 F-THYRO1000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGENIC REG



ION.//0.94:61:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39725  
 F-THYRO1000585//SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLI  
 NG FACTOR SRP55).//0.050:104:36//HOMO SAPIENS (HUMAN).//Q13247  
 F-THYRO1000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP  
 34.5).//0.99:37:40//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P373  
 19  
 F-THYRO1000602//EAMZP30-47 PROTEIN (FRAGMENT).//0.88:61:34//EIMERIA ACER  
 VULINA.//P21959  
 F-THYRO1000605//SUPPRESSOR PROTEIN SRP40.//0.0016:116:26//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32583  
 F-THYRO1000625//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.4e-33:88:78/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1000637//METALLOTHIONEIN A (MT A).//1.0:23:43//SPARUS AURATA (GIL  
 THEAD SEA BREEM).//P52727  
 F-THYRO1000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN.//0.99:26:46//CYANID  
 IUM CALDARIUM (GALDIERIA SULPHURARIA).//019925  
 F-THYRO1000658//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.5e-49:116:69  
 //HOMO SAPIENS (HUMAN).//P39189  
 F-THYRO1000662//DNA-DAMAGE-INDUCIBLE PROTEIN P.//3.7e-15:119:43//ESCHERI  
 CHIA COLI.//Q47155  
 F-THYRO1000666//KINESIN-LIKE PROTEIN KLP1.//1.0e-44:232:41//CHLAMYDOMONA  
 S REINHARDTII.//P46870  
 F-THYRO1000676//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.1e-15:144:39  
 //HOMO SAPIENS (HUMAN).//P39193  
 F-THYRO1000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGENIC REG  
 ION.//0.00033:84:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53129  
 F-THYRO1000699//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.97:20:85//HO  
 MO SAPIENS (HUMAN).//P39192  
 F-THYRO1000712//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.2e-10:69:59//

HOMO SAPIENS (HUMAN).//P39188  
 F-THYRO1000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4  
 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.6e-10:204:32//  
 HOMO SAPIENS (HUMAN).//P04280  
 F-THYRO1000734  
 F-THYRO1000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-46:130:7  
 0//HOMO SAPIENS (HUMAN).//043295  
 F-THYRO1000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERAS  
 E (EC 2.4.99.-) (ST6GALNACIII) (STY).//1.1e-06:95:31//RATTUS NORVEGICUS  
 (RAT).//Q64686  
 F-THYRO1000777//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0031:119:34//HAEMONCH  
 US CONTORTUS.//P16252  
 F-THYRO1000783//MYOSIN IC HEAVY CHAIN.//0.0014:121:37//ACANTHAMOEBA CAST  
 ELLANII (AMOEBA).//P10569  
 F-THYRO1000787//HUNCHBACK PROTEIN (FRAGMENT).//0.54:25:52//PHOLCUS PHALA  
 NGIOIDES.//Q02031  
 F-THYRO1000793//PRE-MRNA SPLICING FACTOR PRP9.//0.91:30:36//SACCHAROMYCE  
 S CEREVISIAE (BAKER'S YEAST).//P19736  
 F-THYRO1000796  
 F-THYRO1000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0  
 .081:31:38//HUMAN ADENOVIRUS TYPE 41.//P23691  
 F-THYRO1000815//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//6.0e-30:81:70/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-THYRO1000829//NEUROTOXIN III (BOM III).//0.022:32:34//BUTHUS OCCITANUS  
 MARDOCHEI (MOROCCAN SCORPION).//P13488  
 F-THYRO1000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGENIC REGI  
 ON (ORF 109).//0.98:25:44//BACTERIOPHAGE P22.//P26750  
 F-THYRO1000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//7.3e-09:83  
 :42//VOLVOX CARTERI.//P21997

F-THYRO1000855//ANTIFREEZE PEPTIDE 4 PRECURSOR.//1.0:54:35//PSEUDOPLEURO  
 NECTA AMERICANUS (WINTER FLOUNDER).//P02734  
 F-THYRO1000865//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.2e-17:66:57//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-THYRO1000895//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.0e-12:58:62/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-THYRO1000916//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.0e-32:101:69  
 //HOMO SAPIENS (HUMAN).//P39189  
 F-THYRO1000926//NITROGEN FIXATION REGULATORY PROTEIN.//5.5e-05:108:27//K  
 LEBSIELLA OXYTOCA.//P56267  
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P  
 5C REDUCTASE).//3.9e-50:147:40//HOMO SAPIENS (HUMAN).//P32322  
 F-THYRO1000951//DIHYDROXYACETONE KINASE (EC 2.7.1.29) (GLYCERONE KINASE)  
 .//1.8e-31:136:56//CITROBACTER FREUNDII.//P45510  
 F-THYRO1000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC RE  
 GION.//2.4e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170  
 F-THYRO1000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR.  
 //1.0:35:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32580  
 F-THYRO1000975  
 F-THYRO1000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//1  
 .3e-20:96:51//CAENORHABDITIS ELEGANS.//Q11076  
 F-THYRO1000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN.//  
 0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25160  
 F-THYRO1000988  
 F-THYRO1001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENIC REGI  
 ON.//0.97:60:31//ESCHERICHIA COLI.//P36675  
 F-THYRO1001031//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.5e-18:56:66/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//5.0e-13:

126:35//HOMO SAPIENS (HUMAN).//P31948  
 F-THYRO1001062//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.1e-35:97:79/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1001093//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.4e-13:70:57/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//4.2e-63:2  
 19:63//HOMO SAPIENS (HUMAN).//P98168  
 F-THYRO1001120//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.  
 00068:160:31//HOMO SAPIENS (HUMAN).//Q15427  
 F-THYRO1001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME  
 I.//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263  
 F-THYRO1001133//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.3e-15:59:66//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-THYRO1001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: P  
 EPTIDE P-D] (FRAGMENT).//0.00088:159:29//HOMO SAPIENS (HUMAN).//P10161  
 F-THYRO1001142//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.0e-29:81:71/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1001173//CYTOCHROME C OXIDASE POLYPEPTIDE VIIS (EC 1.9.3.1).//0.8  
 8:51:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P20610  
 F-THYRO1001177//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.0e-24:91:68/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-THYRO1001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2).//7.3e-27:165:39//M  
 US MUSCULUS (MOUSE).//P08043  
 F-THYRO1001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.67:42:42//HOMO  
 SAPIENS (HUMAN).//P02811  
 F-THYRO1001213//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.9e-16:61:68/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1001262//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-36:50:84/  
 /HOMO SAPIENS (HUMAN).//P39193

F-THYRO1001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.62  
:126:30//STREPTOMYCES FRADIAE.//P20186

F-THYRO1001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC RE  
GION.//1.9e-26:208:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888

F-THYRO1001290//GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT).//1.0:31:38//LAMEL  
LIBRACHIA SP. (DEEP-SEA GIANT TUBE WORM).//P20413

F-THYRO1001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.000  
42:105:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

F-THYRO1001320//COLLAGEN ALPHA 1(III) CHAIN.//0.27:57:38//BOS TAURUS (BO  
VINE).//P04258

F-THYRO1001321//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.5e-20:74:64//  
HOMO SAPIENS (HUMAN).//P39188

F-THYRO1001322//HYPOTHETICAL 7.2 KD PROTEIN.//0.66:49:30//VACCINIA VIRUS  
(STRAIN COPENHAGEN).//P21123

F-THYRO1001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8).//0.94:6  
1:36//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01404

F-THYRO1001363//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0025:23:73//H  
OMO SAPIENS (HUMAN).//P39188

F-THYRO1001365//MERSACIDIN PRECURSOR.//0.35:38:42//BACILLUS SP. (STRAIN  
HIL-Y85/54728).//P43683

F-THYRO1001374//PROTEIN VDLD.//1.6e-13:140:31//HELICOBACTER PYLORI (CAMP  
YLOBACTER PYLORI).//O05729

F-THYRO1001401//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.047:43:48//H  
OMO SAPIENS (HUMAN).//P39192

F-THYRO1001403

F-THYRO1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0  
068:26:42//HOMO SAPIENS (HUMAN).//P22531

F-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.1e  
-81:97:83//MUS MUSCULUS (MOUSE).//O70503

F-THYRO1001411//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.9e-26:89:74/  
/HOMO SAPIENS (HUMAN).//P39193

F-THYRO1001426//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-09:55:61/  
/HOMO SAPIENS (HUMAN).//P39193

F-THYRO1001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-4).//0.68:44:34//BOS TAU  
RUS (BOVINE).//P46162

F-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HE  
AVY CHAIN, TYPE B) (NMMHC-B).//3.8e-64:216:62//HOMO SAPIENS (HUMAN).//P3  
5580

F-THYRO1001480//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.3e-29:88:75/  
/HOMO SAPIENS (HUMAN).//P39194

F-THYRO1001487//HOMEBOX PROTEIN HOX-B4 (HOX-2.6).//0.99:59:37//MUS MUSC  
ULUS (MOUSE).//P10284

F-THYRO1001534//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.4e-14:40:82/  
/HOMO SAPIENS (HUMAN).//P39194

F-THYRO1001537//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FL05 INTERGENIC REG  
ION.//2.4e-07:142:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892

F-THYRO1001541//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.98:26:61//HO  
MO SAPIENS (HUMAN).//P39195

F-THYRO1001559//PROTEIN Q300.//2.6e-05:20:75//MUS MUSCULUS (MOUSE).//Q02  
722

F-THYRO1001570

F-THYRO1001573//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.033:  
71:36//MUS MUSCULUS (MOUSE).//P15265

F-THYRO1001584//SUPPRESSOR PROTEIN SRP40.//2.1e-05:188:27//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P32583

F-THYRO1001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)  
.//6.1e-21:35:91//HOMO SAPIENS (HUMAN).//Q15404

F-THYRO1001602//TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH.//1.0:57:42//HA

EMOPHILUS INFLUENZAE.//P44843  
 F-THYRO1001605//VENOM BASIC PROTEASE INHIBITORS IX AND VIIIB.//1.0:34:38  
 //BUNGARUS FASCIATUS (BANDED KRAIT).//P25660  
 F-THYRO1001617//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.0e-18:55:81/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1001637//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.00020:25:80/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-THYRO1001656//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0091:54:42//MUS  
 MUSCULUS (MOUSE).//P05142  
 F-THYRO1001661//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGI  
 ON (0182).//0.033:77:35//ESCHERICHIA COLI.//P09160  
 F-THYRO1001671//(2'-5')OLIGOADENYLATE SYNTHETASE 1 (EC 2.7.7.-) ((2-5')O  
 LIGO(A) SYNTHETASE 1) (2-5A SYNTHETASE 1) (P46/P41) (E18/E16).//4.3e-34:  
 207:34//HOMO SAPIENS (HUMAN).//P00973  
 F-THYRO1001673//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.9e-08:49:65/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1001703//HYPOTHETICAL 69.8 KD PROTEIN IN BDF1-SFP1 INTERGENIC REG  
 ION.//6.4e-16:134:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06053  
 F-THYRO1001706  
 F-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-27:191:36//DRO  
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-THYRO1001738//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (  
 PROTEIN KINASE A INTERFERENCE PROTEIN).//0.0032:105:32//SACCHAROMYCES CE  
 REVISIAE (BAKER'S YEAST).//P36027  
 F-THYRO1001745  
 F-THYRO1001746//GENE 10 PROTEIN.//1.0:55:30//SPIROPLASMA VIRUS SPV1-R8A2  
 B.//P15901  
 F-THYRO1001772//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.2e-05:41:63//  
 HOMO SAPIENS (HUMAN).//P39188

F-THYRO1001793//HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III./  
/1.5e-26:161:42//CAENORHABDITIS ELEGANS.//P41880

F-THYRO1001809//LATENCY-RELATED PROTEIN 2.//0.49:74:27//HERPES SIMPLEX V  
IRUS (TYPE 1 / STRAIN F).//P17589

F-THYRO1001828//PROTEINASE INHIBITOR.//0.11:34:50//SOLANUM MELONGENA (EG  
GPLANT) (AUBERGINE).//P01078

F-THYRO1001854//ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDIN  
G INHIBITOR HOMOLOG) (DBI).//0.63:50:38//RANA RIDIBUNDA (LAUGHING FROG)  
(MARSH FROG).//P45883

F-THYRO1001895//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.1e-09:72:47//  
HOMO SAPIENS (HUMAN).//P39188

F-THYRO1001907//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGME  
NT).//0.79:36:44//TRYPANOSOMA CRUZI.//Q26327

F-VESEN1000122//HOMEBOX PROTEIN HB9.//0.57:64:32//HOMO SAPIENS (HUMAN).  
//P50219

F-Y79AA1000013//METALLOTHIONEIN B (MT-B).//0.034:35:48//SALMO SALAR (ATL  
ANTIC SALMON).//P52720

F-Y79AA1000033//CHOLECYSTOKININ.//0.97:49:30//PSEUDEMYSS SCRIPTA (SLIDER  
TURTLE).//P80345

F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//1.4e-23:80:60//HOMO SAPIENS  
(HUMAN).//P35226

F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00  
75:127:36//STREPTOMYCES FRADIAE.//P20186

F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P  
EPTIDE P-D] (FRAGMENT).//0.022:135:29//HOMO SAPIENS (HUMAN).//P10162

F-Y79AA1000131//REGULATORY PROTEIN E2.//1.1e-05:175:26//HUMAN PAPILLOMAV  
IRUS TYPE 24.//P50770

F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.4e-06:187:29//M  
US MUSCULUS (MOUSE).//P05143



F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//6.2e-09:4  
7:53//OWENIA FUSIFORMIS.//P21260

F-Y79AA1000214//HISTONE H2A VARIANT.//1.7e-50:107:100//GALLUS GALLUS (CH  
ICKEN).//P02272

F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE  
RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBE  
RIN I).//0.27:64:34//HOMO SAPIENS (HUMAN).//P01148

F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12.//2.5e-72:277:53  
//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//004658

F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.8e-08:174:35//MU  
S MUSCULUS (MOUSE).//P05142

F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.00020:176:33/  
/RATTUS NORVEGICUS (RAT).//P13941

F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III./  
/0.092:127:21//CAENORHABDITIS ELEGANS.//Q09260

F-Y79AA1000328//SEL-10 PROTEIN.//5.3e-05:129:28//CAENORHABDITIS ELEGANS.  
//Q93794

F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).  
//1.0:73:30//OVIS ARIES (SHEEP).//P26372

F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).  
//1.8e-95:205:83//BOS TAURUS (BOVINE).//P53620

F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.036:37:54//PSEUDOPLEU  
RONECTA AMERICANUS (WINTER FLOUNDER).//P02734

F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME III.  
//0.0031:106:28//CAENORHABDITIS ELEGANS.//Q10120

F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.4e-16:  
208:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343

F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTEN  
NA PIGMENT PROTEIN, ALPHA CHAIN C) (LH II-C ALPHA).//0.98:50:30//RHODOPS

EUDOMONAS PALUSTRIS.//P35103  
 F-Y79AA1000410//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.9e-20:62:79/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC REG  
 ION.//1.4e-06:86:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53970  
 F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F44B9.5 IN CHROMOSOME III./  
 /2.8e-34:211:40//CAENORHABDITIS ELEGANS.//P34426  
 F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//3  
 .9e-15:90:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414  
 F-Y79AA1000538//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.37:41:48//HO  
 MO SAPIENS (HUMAN).//P39195  
 F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI  
 NG FACTOR SRP75).//1.8e-21:190:37//HOMO SAPIENS (HUMAN).//Q08170  
 F-Y79AA1000540//SPERM PROTAMINE P1.//0.00045:66:45//DASYURUS VIVERRINUS  
 (SOUTHEASTERN QUOLL), AND DASYURUS HALLUCATUS.//P42135  
 F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALP  
 HA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADA  
 PTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.6e-79:186:87//MUS MUSCULUS (MO  
 USE).//P17427  
 F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.-.-.-) (FRAGMENT).//0.  
 010:35:60//STREPTOMYCES PEUCETIUS.//P32009  
 F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27  
 :197:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320  
 F-Y79AA1000627//ZINC FINGER PROTEIN 134.//1.6e-34:191:35//HOMO SAPIENS (  
 HUMAN).//P52741  
 F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC R  
 EGION.//8.7e-36:250:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P3138  
 0  
 F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A

).//0.00037:108:27//CANDIDA BOIDINII (YEAST).//Q00316  
 F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III./  
 /1.0e-23:210:34//CAENORHABDITIS ELEGANS.//Q09316  
 F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRN  
 P X) (CBP).//1.4e-53:156:68//MUS MUSCULUS (MOUSE).//Q61990  
 F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC RE  
 GION.//1.2e-11:231:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38205  
 F-Y79AA1000782//CUTICLE COLLAGEN 2.//0.012:56:35//CAENORHABDITIS ELEGANS  
 .//P17656  
 F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.3e-08:82:39//P  
 LASMODIUM LOPHURAE.//P04929  
 F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
 .//0.043:13:53//HOMO SAPIENS (HUMAN).//P30808  
 F-Y79AA1000800//PRIA PROTEIN PRECURSOR.//0.031:94:34//LENTINULA EDODES (  
 SHIITAKE MUSHROOM) (LENTINUS EDODES).//Q01200  
 F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC REG  
 ION.//0.26:186:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53882  
 F-Y79AA1000805//AMP. DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE).//0.  
 99:78:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P50998  
 F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REG  
 ION.//3.4e-44:111:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234  
 F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN.//0.0046:187:33//EPSTEIN-BARR  
 VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//1.0e-75:239:66//CRICETULUS GRISE  
 US (CHINESE HAMSTER).//P05209  
 F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.  
 0078:57:31//HOMO SAPIENS (HUMAN).//P22532  
 F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//8.5e-11:241:  
 26//GALLUS GALLUS (CHICKEN).//P10587

F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.69:12  
2:31//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-  
2B GDP-GTP EXCHANGE FACTOR).//3.3e-102:211:93//RATTUS NORVEGICUS (RAT)./  
/P70541

F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:67:38//GALL  
US GALLUS (CHICKEN).//P02457

F-Y79AA1000976//INVOLUCRIN.//0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED  
CAPUCHIN).//P24709

F-Y79AA1000985//PERICENTRIN.//1.1e-24:116:59//MUS MUSCULUS (MOUSE).//P48  
725

F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC RE  
GION.//0.37:79:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38250

F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE  
SP1].//0.93:43:39//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80001

F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURS  
OR (EC 1.3.99.-) (VLCAD).//1.5e-51:211:52//BOS TAURUS (BOVINE).//P48818

F-Y79AA1001061//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-25:85:69/  
/HOMO SAPIENS (HUMAN).//P39194

F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHOND  
ROCALCIN].//0.0015:207:33//MUS MUSCULUS (MOUSE).//P28481

F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9)./  
/0.99:36:41//ARANEUS DIADEMATUS (SPIDER).//P80515

F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.  
//1.0e-06:197:23//CAENORHABDITIS ELEGANS.//P34492

F-Y79AA1001105//HOMEBOX PROTEIN OTX2.//2.9e-62:163:79//MUS MUSCULUS (MO  
USE).//P80206

F-Y79AA1001145//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.024:42:59//H  
OMO SAPIENS (HUMAN).//P39195

F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC REGION.//0.96:20:50//AUTOGRAPHICA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV).//P41471

F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN.//3.9e-05:135:34//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.00017:93:38//CAENORHABDITIS ELEGANS.//Q09456

F-Y79AA1001211

F-Y79AA1001216//TENSIN.//0.012:134:32//GALLUS GALLUS (CHICKEN).//Q04205

F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.088:75:34//HOMO SAPIENS (HUMAN).//Q02817

F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//1.1e-40:139:51//RATTUS NORVEGICUS (RAT).//P51657

F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//2.0e-22:108:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38238

F-Y79AA1001281

F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0022:49:44//MUS MUSCULUS (MOUSE).//P05143

F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR.//0.98:117:25//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P92959

F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.082:44:40//SUS SCROFA (PIG).//P35323

F-Y79AA1001384//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.99:47:40//MUS MUSCULUS (MOUSE).//P33622

F-Y79AA1001391//HOMEODOMAIN PROTEIN HOX-A13 (HOX-1J).//9.8e-58:157:62//HOMO SAPIENS (HUMAN).//P31271

F-Y79AA1001394//TRICHOHYALIN.//4.7e-08:121:36//HOMO SAPIENS (HUMAN).//Q0

7283

F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF.//0.0087:81:33//MUS MUSCULUS (MOUSE).//P70459

F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//4.5e-21:125:44//CAENORHABDITIS ELEGANS.//Q11076

F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.3e-17:249:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313

F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I 49 KD POLYPEPTIDE (EC 2.7.7.6) (A49).//0.0099:155:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q01080

F-Y79AA1001541

F-Y79AA1001548//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-17:53:83//HOMO SAPIENS (HUMAN).//P39192

F-Y79AA1001555//MAJOR SURFACE ANTIGEN.//0.046:62:29//HEPATITIS B VIRUS.//P31873

F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//8.6e-11:144:31//ESCHERICHIA COLI.//P27550

F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.012:64:40//MUS MUSCULUS (MOUSE).//P15265

F-Y79AA1001594//CORNIFIN BETA.//0.61:88:31//MUS MUSCULUS (MOUSE).//009116

F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.024:170:30//HOMO SAPIENS (HUMAN).//000268

F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//4.5e-09:136:27//HOMO SAPIENS (HUMAN).//P28698

F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.093:94:26//MYCOBACTERIUM TUBERCULOSIS.//P71779

F-Y79AA1001665//HOMEBOX PROTEIN DLX-2 (HOMEBOX PROTEIN TES-1).//0.79:9  
0:26//MUS MUSCULUS (MOUSE).//P40764

F-Y79AA1001679//LAMBDA-CRYSTALLIN.//1.6e-95:224:81//ORYCTOLAGUS CUNICULU  
S (RABBIT).//P14755

F-Y79AA1001692//GERM CELL-LESS PROTEIN.//3.5e-08:78:38//DROSOPHILA MELAN  
OGASTER (FRUIT FLY).//Q01820

F-Y79AA1001696//INSULIN.//1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL).//  
P42633

F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN.//0.0013:192:33//EPSTEIN-BARR  
VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-Y79AA1001711//PARATHYMOSIN (ZINC-BINDING 11.5 KD PROTEIN).//0.032:38:3  
4//RATTUS NORVEGICUS (RAT).//P04550

F-Y79AA1001781

F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0063:12  
8:30//HOMO SAPIENS (HUMAN).//P50552

F-Y79AA1001827//SPERM PROTAMINE P1.//0.015:45:40//DIDELPHIS MARSUPIALIS  
VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TA  
ILED GREY OPOSSUM).//P35305

F-Y79AA1001846//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-09:42:73//  
HOMO SAPIENS (HUMAN).//P39188

F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT).//1.8e-10:63:44//PSYCHODA CI  
NEREA.//Q02035

F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK1  
0).//0.00036:108:37//MUS MUSCULUS (MOUSE).//Q61967

F-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPT  
IONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//3.2e-07:100  
:35//HOMO SAPIENS (HUMAN).//P43489

F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.020:25:6  
4//HOMO SAPIENS (HUMAN).//P20931

F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P  
EPTIDE P-D] (FRAGMENT).//0.016:83:36//HOMO SAPIENS (HUMAN).//P10162

F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELI  
CASE SPAC10F6.02C.//8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YE  
AST).//042643

F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBI  
QUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.8e-39:143  
:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743

F-Y79AA1002083//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
.//0.036:53:45//HOMO SAPIENS (HUMAN).//P30808

F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN F02A9.4 IN CHROMOSOME III./  
/0.12:171:22//CAENORHABDITIS ELEGANS.//P34384

F-Y79AA1002093//MAX PROTEIN.//3.1e-07:111:29//BRACHYDANIO RERIO (ZEBRAFI  
SH) (ZEBRA DANIO).//P52161

F-Y79AA1002103//SHORT NEUROTOXIN C.//0.040:21:47//AIPYSURUS LAEVIS (OLIV  
E SEA SNAKE).//P19958

F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827.//0.84:68:30//METHANOCOCCUS  
JANNASCHII.//Q58237

F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC  
REGION.//3.4e-29:197:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40  
206

F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//1.9e-19:120:45//DROSOPH  
ILA MELANOGASTER (FRUIT FLY).//Q24133

F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6).//0.0011:162:32//MUS MUSC  
ULUS (MOUSE).//P70327

F-Y79AA1002208//ANKYRIN.//2.9e-08:231:29//MUS MUSCULUS (MOUSE).//Q02357

F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE; MITOCHONDRIAL PRECURSOR (EC 6.1  
.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//3.7e-23:170:32//SACCHAROMYCES CE  
REVISIAE (BAKER'S YEAST).//P48527



F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPR K).//0.0061:69:31//HOMO SAPIENS (HUMAN).//P35321

F-Y79AA1002211//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//9.2e-10:43:62//HOMO SAPIENS (HUMAN).//P39193

F-Y79AA1002220

F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I./ /1.9e-21:147:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264

F-Y79AA1002234

F-Y79AA1002246//MYOSIN IC HEAVY CHAIN.//0.00066:131:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III. //4.3e-45:164:48//CAENORHABDITIS ELEGANS.//Q02328

F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0063:99:31//HOMO SAPIENS (HUMAN).//P10161

F-Y79AA1002307

F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III. //0.75:198:24//CAENORHABDITIS ELEGANS.//P46012

F-Y79AA1002351//CUTICLE COLLAGEN 34.//0.74:128:35//CAENORHABDITIS ELEGANS.//P34687

F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2.//0.050:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40036

F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//1.0:89:30//CARASSIUS AURATUS (GOLDFISH).//P17691

F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION.//3.7e-16:232:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53899

F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//6.7e-72:162:84//HOMO SAPIENS (HUMAN).//P17812

F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.8

1:34:41//HOMO SAPIENS (HUMAN).//P22531  
F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68.//0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558  
F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35).//2.3e-60:217:44//MUS MUSCULUS (MOUSE).//P15620  
F-Y79AA1002482//ZINC FINGER PROTEIN 141.//2.0e-31:90:55//HOMO SAPIENS (HUMAN).//Q15928  
F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

【 0 8 2 5 】

相同性検索結果データ 2.

5' 末端クローン配列に対するESTとSTSを除いたGenBank相同性検索結果データ

各データは

クローン配列名、

トップヒットデータのDefinition、

P値:比較配列の長さ (base):相同性(%),

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds  
./3.4e-106:695:86//L16953

F-HEMBA1000012//Caenorhabditis elegans cosmid C16C10, complete sequence.  
//1.5e-24:374:66//Z46787

F-HEMBA1000020//Homo sapiens beta 2 gene.//3.5e-112:529:90//X02344

F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein (GIT1) mRNA, complete cds.//5.6e-124:743:88//AF085693

F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-25:529:65//AC004581

F-HEMBA1000046//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING DRAFT SEQUENCE.//3.2e-11:330:63//AL033528

F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS and chromosome 6 fragment, complete sequence.//0.32:407:59//AL022477

F-HEMBA1000076//Homo sapiens full length insert cDNA clone ZB97G06.//6.2e-135:594:98//AF086182

F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sapiens genomic clone 2291M18, genomic survey sequence.//2.8e-16:132:79//AQ004134

F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//8.6e-98:230:93//AC003104

F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.1e-167:791:98//AB018340

F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds.//2.2e-44:242:96//AB018331

F-HEMBA1000156//Rattus norvegicus scaffold attachment factor B mRNA, complete cds.//1.1e-10:409:60//AF056324

F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds.//1.6e-35:365:73//U80741

F-HEMBA1000168//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//0.99:290:61//AL031033

F-HEMBA1000180//rat u2 small nuclear rna gene and flanks.//3.7e-18:112:98//K00034

F-HEMBA1000185

F-HEMBA1000193//Human FMR1 gene, 5' end.//0.0012:191:67//L19476

F-HEMBA1000201//Human Inil mRNA, complete cds.//2.0e-73:440:92//U04847

F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence.//0.90:332:59//AL034559

F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA,

complete cds.//4.8e-117:585:83//AF060194  
F-HEMBA1000227//H.sapiens CpG island DNA genomic MseI fragment, clone 17  
9h6, reverse read cpg179h6.rtl1a.//1.9e-14:95:98//Z64921  
F-HEMBA1000231//H.sapiens CpG island DNA genomic MseI fragment, clone 90  
a5, reverse read cpg90a5.rtl1a.//5.1e-34:186:97//Z56144  
F-HEMBA1000243//Human DNA sequence from PAC 440021 on chromosome X conta  
ins ESTs and STS.//4.1e-67:291:82//Z84481  
F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroid ankyrin.//0.029:316:  
59//X69065  
F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, com  
plete sequence.//0.35:467:60//AC004454  
F-HEMBA1000264  
F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2  
unordered pieces.//8.9e-20:218:78//AC004825  
F-HEMBA1000282//Homo sapiens chromosome Y, clone 264,M,20, complete sequ  
ence.//4.2e-08:134:77//AC004617  
F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens genomic clone A-345L05  
, genomic survey sequence.//1.1e-06:152:73//B17459  
F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds.//3.2e-  
11:507:62//M33764  
F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sapiens genomic clone 21  
69N13, genomic survey sequence.//5.4e-06:86:88//B90730  
F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//  
7.9e-111:701:86//AF030131  
F-HEMBA1000304//HS\_3006\_A1\_A09\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey  
sequence.//5.2e-40:240:92//AQ118226  
F-HEMBA1000307//Mus musculus mRNA for CDV-1R protein.//7.9e-127:815:84//  
Y10495

F-HEMBA1000327//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.4e-11:87:96//AQ187492

F-HEMBA1000333

F-HEMBA1000338//Homo sapiens chromosome X, PAC 671D9, complete sequence.//4.0e-66:271:84//AF031078

F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.64:334:60//AC004848

F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds.//0.017:313:63//U25056

F-HEMBA1000356//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.87:198:61//L40178

F-HEMBA1000357//HS\_3194\_A1\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//6.5e-90:436:98//AQ173748

F-HEMBA1000366//HS\_3027\_B2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence.//0.0074:192:64//AQ128843

F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//4.2e-106:133:99//AL031587

F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.6e-22:659:63//AC006116

F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPCI11-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces.//3.2e-06:136:75//AC006122

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence.//3.5e-111:284:95//AC004520

F-HEMBA1000392//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//1.8e-39:332:80//AL031984

F-HEMBA1000396//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//9.5e-35:364:73//U80460

F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409

F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584

F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112

F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554

F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393

F-HEMBA1000442

F-HEMBA1000456//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//6.3e-06:62:96//B85188

F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808

F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//AC004839

F-HEMBA1000464//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.8e-25:397:72//AC006213

F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 2167P21, genomic survey sequence.//4.0e-83:406:99//B94160

F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT Region, complete sequence.//4.2e-53:312:93//AC004033

F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y

13334

F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-06:338:58//X00740

F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//9.4e-41:591:69//AC005884

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666

F-HEMBA1000505

F-HEMBA1000508//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661

F-HEMBA1000518//Caenorhabditis elegans cosmid C17H12.//0.96:425:58//AF045642

F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616

F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006

F-HEMBA1000523

F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.//3.9e-35:290:80//U08215

F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177\_H\_5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973

F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project).//0.057:265:63//AL033545

F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//1.2e-110:572:88//D89340

F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237

F-HEMBA1000555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 134019, WORKING DRAFT SEQUENCE.//3.2e-175:838:98//AL034555  
 F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP Homo sapiens genomic clone 23  
 69F15, genomic survey sequence.//2.8e-32:315:78//AQ074611  
 F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein  
 Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U  
 92564  
 F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomi  
 c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC  
 005504  
 F-HEMBA1000568//HS\_3243\_B2\_A12\_MR CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey  
 sequence.//3.1e-54:323:91//AQ219628  
 F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein.//1.4e-19:440:6  
 1//X89571  
 F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic  
 sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0016:557:57//A  
 C005506  
 F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete  
 cds.//1.7e-11:132:79//AF045573  
 F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.3  
 e-43:228:97//AJ007509  
 F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence.//7.  
 3e-07:68:94//AF046733  
 F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contai  
 ns ESTs.//8.7e-71:553:79//Z83822  
 F-HEMBA1000604//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 237J2, WORKING DRAFT SEQUENCE.//2.9e-21:158:75//AL021394  
 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.  
 1e-118:561:99//AB007925



F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//2.2e-28:426:70//AC004382  
F-HEMBA1000636//Human CpG island sequence, clone Q28B8.//1.0e-15:274:68/D85773  
F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//6.7e-137:639:99//AB014590  
F-HEMBA1000655//, complete sequence.//5.1e-83:685:80//AC005815  
F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.1e-91:597:84//U35776  
F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.019:695:57//AC004907  
F-HEMBA1000673//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//1.5e-48:325:85//Z86090  
F-HEMBA1000682//Homo sapiens (subclone 5\_g5 from P1 H25) DNA sequence.//7.7e-61:615:74//L43411  
F-HEMBA1000686  
F-HEMBA1000702  
F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0037:569:57//AC005507  
F-HEMBA1000719//Streptomyces coelicolor cosmid 1C2.//2.0e-09:483:62//AL031124  
F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome.//0.00058:762:57//U87145  
F-HEMBA1000726//H.sapiens HLA-DRB1\*15 gene.//9.8e-49:189:89//X88791  
F-HEMBA1000727//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0054:206:67//B60158  
F-HEMBA1000747  
F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.

31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.3e-05:124:75//AL024509

F-HEMBA1000752//Human Chromosome X, complete sequence.//5.9e-48:502:75//AC004073

F-HEMBA1000769//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.011:179:67//AC005043

F-HEMBA1000773//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone Y59A8, WORKING DRAFT SEQUENCE.//0.070:231:63//Z98870

F-HEMBA1000774//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//6.2e-40:385:75//AC004953

F-HEMBA1000791

F-HEMBA1000817//Myrmecia pilosula HI87-135 mitochondrion cytochrome b gene, partial cds.//0.99:244:58//U15678

F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//0.033:294:62//Z81370

F-HEMBA1000827//Borrelia burgdorferi (section 50 of 70) of the complete genome.//9.7e-05:463:58//AE001164

F-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//3.0e-153:732:98//AL022394

F-HEMBA1000851//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//1.6e-31:386:72//AF059273

F-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park

Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.5e-115:455:98//AC005295

F-HEMBA1000867

F-HEMBA1000869//Human DNA sequence from cosmid J138017, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//6.6e-41:424:75//Z72519

F-HEMBA1000870//Gnamptodon pumilio cytochrome oxidase II gene, partial cds; and tRNA-Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitochondrial genes for mitochondrial products.//0.0049:211:66//AF034598

F-HEMBA1000872//CIT-HSP-2355D20.TF CIT-HSP Homo sapiens genomic clone 2355D20, genomic survey sequence.//3.7e-33:180:98//AQ059583

F-HEMBA1000876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//5.6e-37:262:72//Z83826

F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1) mRNA, complete cds.//1.0:304:59//AF015523

F-HEMBA1000910//M.musculus necdin mRNA, complete cds.//6.1e-08:256:61//M80840

F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eliminated sequence region.//0.13:232:63//U88158

F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds.//1.0:213:65//U00147

F-HEMBA1000934//CIT-HSP-2053H24.TR CIT-HSP Homo sapiens genomic clone 2053H24, genomic survey sequence.//5.5e-11:275:64//B69224

F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15 unordered pieces.//9.7e-05:78:83//AC004878

F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//5.8e-140:661:99//AC005324

F-HEMBA1000946

F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12

unordered pieces.//8.3e-16:181:75//AC004967  
F-HEMBA1000968//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 69M21, WORKING DRAFT SEQUENCE.//4.4e-117:398:86//AL031735  
F-HEMBA1000971//H.sapiens CpG island DNA genomic MseI fragment, clone 182f4, forward read cpg182f4.ft1a.//1.5e-20:126:96//Z57528  
F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.34:642:59//AB020858  
F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//5.1e-183:865:98//AC004817  
F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, complete cds.//0.00065:391:62//M30023  
F-HEMBA1000985//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSS, GSSs and a CA repeat polymorphism, complete sequence.//3.4e-05:243:65//Z93929  
F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genomic sequence.//6.6e-06:508:61//AD000813  
F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds.//1.2e-22:193:84//D84064  
F-HEMBA1001007  
F-HEMBA1001008//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//7.8e-46:532:73//AL031577  
F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence.//0.97:369:59//X17115  
F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//4.4e-139:661:98//AB007937  
F-HEMBA1001019//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//1.6

e-16:521:64//AC006213

F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178\_C\_3, complete sequence.//3.8e-50:367:72//AC005702

F-HEMBA1001022

F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence.//5.0e-23:378:69//AE000658

F-HEMBA1001026//Homo sapiens DNA sequence from PAC 435D1 on chromosome X q25. Contains ESTs and STS.//7.6e-19:867:60//Z86064

F-HEMBA1001043//HS\_2219\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence.//3.0e-15:124:88//AQ301521

F-HEMBA1001051//Human Chromosome X clone bWDX342, complete sequence.//4.8e-79:308:84//AC004072

F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.53:384:61//AC005341

F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084

F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence.//0.98:280:62//AC006079

F-HEMBA1001071//Human mRNA for pro alpha 1 (III) collagen C-terminal propeptide.//1.1e-31:181:96//X01742

F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 3951 nt].//3.6e-13:338:65//S78219

F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9.//0.00012:364:63//AL034446

F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586

F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//I258  
63

F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-11  
9:609:96//AC005105

F-HEMBA1001099

F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complet  
e sequence.//2.4e-58:347:87//AC005250

F-HEMBA1001121//Human DNA sequence.\*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723

F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of  
the complete sequence.//9.2e-07:732:57//AE001383

F-HEMBA1001123//Homo sapiens full length insert cDNA clone ZD38E12.//1.1  
e-11:231:68//AF086247

F-HEMBA1001133//Homo sapiens clone DJ0856024, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//0.011:163:69//AC004909

F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds.//6  
.9e-72:527:77//AB018341

F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 u  
nordered pieces.//2.3e-120:578:98//AC005077

F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 geno  
mic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59/  
/AC005507

F-HEMBA1001174//R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like pro  
tein 5.//1.0e-59:565:73//X78604

F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unord  
ered pieces.//0.0037:151:70//AC004815

F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequenc  
e.//7.4e-35:195:81//AC002410

F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence.//1.9e-1

71:826:98//AC004917

F-HEMBA1001226//Homo sapiens clone DJ0850I01, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.00010:557:57//AC006009

F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601\_N\_13, complete sequence.//0.0086:372:58//AC005389

F-HEMBA1001247//H.sapiens CpG island DNA genomic MseI fragment, clone 11 b11, reverse read cpg11b11.rtl1a.//2.0e-24:154:93//Z64441

F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-88:659:81//AF047020

F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205

F-HEMBA1001281

F-HEMBA1001286//B.taurus mRNA for RF-36-DNA-binding protein.//7.7e-26:236:81//X15543

F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.5e-28:530:64//AC004131

F-HEMBA1001294//Yeast mitochondrial aap1 gene for ATPase subunit 8.//2.8e-15:722:60//X00960

F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//AL031003

F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//7.2e-121:439:96//E12260

F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505

F-HEMBA1001310//HS\_3252\_B2\_B12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic survey sequence.//1.2e-16:166:82//AQ217054

F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 203

4J6, genomic survey sequence.//0.33:256:59//B79408  
F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.  
//7.8e-30:165:99//L20861  
F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6  
. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a  
beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE ps  
eudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudo  
gene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences)  
and a CA repeat polymorphism, complete sequence.//5.4e-19:347:68//AL021  
368  
F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 23  
54E10, genomic survey sequence.//0.012:152:65//AQ075713  
F-HEMBA1001330//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from contig 3-103, complete sequence.//0.0037:254:62//AL010208  
F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)  
mRNA, complete cds.//1.1e-103:516:97//AF057358  
F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete  
sequence.//1.7e-150:706:99//AC006241  
F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6.//1.0:375:59//AL03350  
5  
F-HEMBA1001377//HS\_3020\_B1\_D12\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3020 Col=23 Row=H, genomic survey  
sequence.//0.00022:63:77//AQ105297  
F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of  
the complete sequence.//0.00035:317:60//AE001431  
F-HEMBA1001387//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey s  
equence.//5.0e-90:437:98//AQ155035  
F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15



unordered pieces.//4.2e-47:159:89//AC005073

F-HEMBA1001391//Human DNA sequence from clone 409010 on chromosome 20q12

Contains CA repeat, GSS, STS, complete sequence.//2.0e-06:495:60//AL031256

F-HEMBA1001398//H.sapiens CpG island DNA genomic MseI fragment, clone 70d11, forward read cpg70d11.ft1b.//0.018:46:97//Z62591

F-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380

F-HEMBA1001407//Mus musculus domesticus Torino (Sry) gene, complete cds.//0.36:363:57//U03645

F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic survey sequence.//8.4e-12:516:60//AG001050

F-HEMBA1001413

F-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//0.98:177:64//AL031732

F-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.0e-177:859:97//AC006146

F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence.//2.0e-35:376:64//AC004917

F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//1.2e-74:284:84//AC005670

F-HEMBA1001442//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-66, complete sequence.//0.056:194:63//AL010138

F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//0.96:328:61//AC004047

F-HEMBA1001450

F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB. ESTs and STS, complete sequence.//2.0e-47:468:73//AL031115

F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sapiens genomic clone 32J2, genomic survey sequence.//1.5e-05:223:65//B78859

F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652

F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:99//AB011144

F-HEMBA1001478//HS\_2228\_A2\_B03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-40:275:88//AQ032041

F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSS, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//7.7e-47:311:85//AL031133

F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//2.0e-130:699:93//U89337

F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete sequence.//4.1e-114:711:85//AC005794

F-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//5.7e-162:769:98//AC004549

F-HEMBA1001522//Caenorhabditis elegans cosmid ZK328.//8.6e-17:498:61//U50193

F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//0.31:120:69//Z98258

F-HEMBA1001533

F-HEMBA1001557//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136

F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1 q23-25. Contains FM02 and FM03 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL021026

F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044

F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//AC004453

F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449

F-HEMBA1001581//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980

F-HEMBA1001585

F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//AC002432

F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918

F-HEMBA1001608//RPCI11-72E2.TJ RPCI11 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131

F-HEMBA1001620//Oryza sativa RINO1 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107

F-HEMBA1001635//HS\_3208\_A1\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944

F-HEMBA1001636//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216

F-HEMBA1001640//HS\_3253\_B2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058

F-HEMBA1001647//H.sapiens gene for plectin.//0.00052:629:61//Z54367

F-HEMBA1001651//Salmo salar DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206.

F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//AC005368

F-HEMBA1001658//M.musculus COL3A1 gene for collagen alpha-I.//2.4e-30:742:62//X52046

F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//AC005740

F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//6.1e-152:725:98//AF072247

F-HEMBA1001675//RPCI11-54F8.TV RPCI11 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.3e-75:341:85//AQ082126

F-HEMBA1001678//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//8.4e-54:551:74//AC002349

F-HEMBA1001681

F-HEMBA1001702//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.94:676:54//AE001398

F-HEMBA1001709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531

F-HEMBA1001711//Lysiphlebus melandriicola NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:413:60//AF069178

F-HEMBA1001712//Homo sapiens BAC clone RG041H04 from 7q21-q22, complete

sequence.//0.091:315:61//AC004519

F-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//1.6e-28:218:75//U12250

F-HEMBA1001718//HS\_3056\_A2\_H08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=16 Row=0, genomic survey sequence.//2.0e-79:383:99//AQ106367

F-HEMBA1001723//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116793

F-HEMBA1001731//HS\_3021\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658

F-HEMBA1001734//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.00060:392:60//AC004617

F-HEMBA1001744//HS\_3194\_A1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163:97//AQ252295

F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59//AC002102

F-HEMBA1001746//HS\_2163\_B1\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238:70//AQ085995

F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198:86//AC002109

F-HEMBA1001781

F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-13:296:65//AC002099

F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//0.18:534:59//AF038

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F-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//2.2e-40:335:80//AQ009222

F-HEMBA1001803//M.musculus (Balb/C) P/L01 mRNA.//1.7e-25:286:74//Z31360

F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977

F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809:98//AB007969

F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:639:57//AJ004801

F-HEMBA1001815

F-HEMBA1001819//HS\_3079\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396:97//AQ186616

F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//0.00026:436:60//AC005013

F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510:65//AF064243

F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:344:68//AF020275

F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.0094:553:58//AC005161

F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//1.2e-22:316:70//AC005867

F-HEMBA1001847//M.musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397:69//X55126

F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865:98//AB014517

F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic se

quence, complete sequence.//0.38:337:62//AC005395

F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224:63//U28735

F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//6.7e-98:288:91//AC005065

F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KVLQT1 gene, complete sequence.//4.9e-114:476:84//AC003693

F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF026954

F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221:63//AC003065

F-HEMBA1001912//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732

F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00063:219:65//AC005766

F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 5/10.//0.00011:366:63//AB020873

F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.//0.00024:562:58//D82031

F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855:99//AF000145

F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kd) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310

F-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5

unordered pieces.//7.5e-175:861:97//AC005629

F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//0.097:107:71//AC006057

F-HEMBA1001945//Drosophila F family transposable element F12 3' region./0.94:140:65//X01934

F-HEMBA1001950//H.sapiens CpG island DNA genomic MseI fragment, clone 15 b5, forward read cpg15b5.ft1q.//1.4e-27:168:95//Z54728

F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010:108:71//AJ000390

F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507

F-HEMBA1001964

F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive iso log of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178

F-HEMBA1001979//HS\_3067\_B1\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506

F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551

F-HEMBA1001991//HS\_2237\_A2\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283

F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950 nt].//2.7e-33:364:74//S90449

F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214



:68//AC005948

F-HEMBA1002018

F-HEMBA1002022//Human p37NB mRNA, complete cds.//0.014:58:96//U32907

F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//  
M17284

F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.  
2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs an  
d GSSs, complete sequence.//0.31:497:58//AL031053

F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192),  
complete sequence.//4.5e-42:532:63//AC005216

F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequen  
ce, complete sequence.//0.81:435:59//AF025422

F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-  
3) mRNA, complete cds.//7.2e-130:769:87//U92703

F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.  
3e-47:124:96//AC004943

F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.  
7e-13:132:71//D83649

F-HEMBA1002113//F.rubripes GSS sequence, clone 063K10bB4, genomic survey  
sequence.//0.029:142:66//Z88840

F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1  
.3e-14:515:62//AC000378

F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNN3)  
mRNA, complete cds.//0.98:222:61//AF031815

F-HEMBA1002139//Caenorhabditis elegans cosmid F55C9, complete sequence./  
/0.0081:371:60//Z81549

F-HEMBA1002144//Saccharomyces cerevisiae mitochondrion transfer RNA-Met  
(tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888

F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.

00017:353:62//AB018263

F-HEMBA1002151

F-HEMBA1002153//CITBI-E1-2519I20.TR CITBI-E1 Homo sapiens genomic clone 2519I20, genomic survey sequence.//8.5e-61:334:94//AQ277613

F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-4:385:77//AC005232

F-HEMBA1002161//Coturnix coturnix slow myosin heavy chain 2 (qmyhc2) mRNA, partial cds.//2.1e-59:571:74//AF006829

F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210

F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712

F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//AC000066

F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00066:466:59//AC004825

F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-23:176:77//AC005015

F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds.//1.0:382:59//AB014589

F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence.//1.8e-20:368:66//AC005150

F-HEMBA1002204//HS\_2055\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=0, genomic survey sequence.//1.2e-06:178:65//AQ235350

F-HEMBA1002212//S.cerevisiae chromosome IV reading frame ORF YDL101c.//0.035:345:60//Z74149

F-HEMBA1002215//M.musculus mRNA for testin.//4.6e-80:504:87//X78989

F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-63:336:74//AC003035

F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//2.6e-39:311:81//AC006044

F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//1.6e-12:397:64//AC004861

F-HEMBA1002241

F-HEMBA1002253

F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds.//3.5e-151:731:97//AF061936

F-HEMBA1002265//Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-qter contains ESTs, STS and endogenous retrovirus.//1.3e-09:313:62//Z71183

F-HEMBA1002267

F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//0.069:495:58//AC006210

F-HEMBA1002321//Homo sapiens PAC clone DJ0991023, complete sequence.//0.019:564:58//AC004944

F-HEMBA1002328//CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone 2387N15, genomic survey sequence.//1.8e-71:346:99//AQ240836

F-HEMBA1002337//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MYN8, complete sequence.//0.84:547:57//AB020754

F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-185:872:98//AB018314

F-HEMBA1002348//CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey sequence.//9.1e-33:230:75//AQ110676

F-HEMBA1002349//Plasmodium falciparum histidine-rich protein II (HRP II) gene, complete cds.//9.4e-06:504:57//U69551

F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//7.3e-188:872:99//AF092563

F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//2.1e-20:262:72//AB020868

F-HEMBA1002389//D.discoideum spore coat 60 (sp60) gene, 5' flank.//0.010:95:73//M34546

F-HEMBA1002417//Canis familiaris ZO-3 (zo-3) mRNA, complete cds.//6.2e-120:767:85//AF023617

F-HEMBA1002419//HS-1047-A1-F01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=1 Row=K, genomic survey sequence.//7.6e-06:111:76//B38165

F-HEMBA1002430//HS\_3137\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence.//1.6e-56:367:88//AQ148697

F-HEMBA1002439//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.67:129:64//M25216

F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds.//1.1e-30:274:72//AF051347

F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-173:822:98//AC005378

F-HEMBA1002462//Sequence 41 from patent US 5708157.//9.8e-51:519:73//I80067

F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds.//4.0e-108:603:92//D50912

F-HEMBA1002475//Streptomyces coelicolor cosmid 2H4.//0.0068:626:57//AL031514

F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//1.5e-40:349:78//AC005034

F-HEMBA1002486

F-HEMBA1002495//HS\_3218\_B1\_A12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=23 Row=B, genomic survey sequence.//1.0:179:67//AQ181410

F-HEMBA1002498//Homo sapiens full length insert cDNA clone ZD76B01.//1.4e-129:619:98//AF086404

F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.9e-24:306:68//AC004873

F-HEMBA1002508//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464:83//AC004799

F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//2.8e-157:738:98//AJ011972

F-HEMBA1002515//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307:64//AL022329

F-HEMBA1002538//HS\_2185\_B2\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2185 Col=8 Row=D, genomic survey sequence.//4.7e-37:339:78//AQ298315

F-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//3.2e-70:372:95//AQ188792

F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//3.5e-137:655:98//AF016903

F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:173:68//U31875

F-HEMBA1002555//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.2e-15:628:60//AC004670

F-HEMBA1002558//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5

(from Lawrence Livermore), complete sequence.//2.3e-41:353:76//AC002366  
 F-HEMBA1002561//Homo sapiens chromosome 17, clone HRPC29G21, complete sequence.//1.1e-39:538:66//AC003687  
 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//1.3e-140:457:99//AF075587  
 F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//5.1e-79:385:99//AQ038102  
 F-HEMBA1002590//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.9e-35:430:70//AC005940  
 F-HEMBA1002592//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//4.4e-19:303:71//Z93403  
 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//4.4e-175:820:99//AB011169  
 F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, complete sequence.//0.14:353:58//AC004413  
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//2.9e-187:632:97//AB018351  
 F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-05:792:58//AC004153  
 F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576:58//AL034446  
 F-HEMBA1002645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222:86//AL031118  
 F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//3.8e-182:859:99//AC004839  
 F-HEMBA1002659//Z.mobilis alcohol dehydrogenase I (adhA) gene, complete cds.//0.97:144:66//M32100

F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, complete sequence.//1.3e-116:774:84//AC004535

F-HEMBA1002666

F-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750:98//AL034421

F-HEMBA1002679//nbxb0002cC12r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517:58//AQ051621

F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete genome.//8.3e-20:651:61//Z86099

F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subunit gene, complete cds.//7.6e-62:306:81//AF060195

F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1.9e-10:327:62//AB007924

F-HEMBA1002712

F-HEMBA1002716//HS\_3064\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491:96//AQ142980

F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//6.1e-21:217:77//AC004782

F-HEMBA1002730//Human platelet glycoprotein IIIa (GPIIIa) gene, exon 1./0.57:125:67//M57481

F-HEMBA1002742//RPCI11-39J10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-39J10, genomic survey sequence.//1.1e-86:414:99//AQ029102

F-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//7.1e-70:303:82//AC003694

F-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//0.096:212:62//AL031732

F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89), complete sequence.//6.7e-40:232:70//AC004622

F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.0e-177:834:98//AB011126

F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.3e-140:840:88//E12829

F-HEMBA1002777//F.rubripes GSS sequence, clone 189C06dB12, genomic survey sequence.//1.1e-28:263:77//AL007965

F-HEMBA1002779//CIT-HSP-2333I1.TF CIT-HSP Homo sapiens genomic clone 2333I1, genomic survey sequence.//1.8e-32:180:98//AQ036891

F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, complete sequence.//7.0e-06:199:67//AC004592

F-HEMBA1002794//H.sapiens mRNA for protein kinase C mu.//0.00015:244:67//X75756

F-HEMBA1002801//Plasmodium falciparum MAL3P2, complete sequence.//0.0010:534:57//AL034558

F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.1e-167:820:97//AF071185

F-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-113:254:90//AC005043

F-HEMBA1002818//Cricetulus griseus H411 precursor (H411) mRNA, complete cds.//1.2e-122:760:86//AF046870

F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.0055:235:65//AL022153

F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.4e-170:744:99//AC004707

F-HEMBA1002850//Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//1.3e-05:334:59//AF069186

F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic clone 2323A16, genomic survey sequence.//2.9e-140:750:93//AQ028419



F-HEMBA1002876//HS\_2270\_B1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=5 Row=P, genomic survey sequence.//0.44:163:64//AQ164031

F-HEMBA1002886

F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence.//0.00015:277:61//AC005195

F-HEMBA1002921

F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic clone 2171H4, genomic survey sequence.//0.0016:175:66//B89715

F-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.2e-169:797:98//AL031681

F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//4.9e-173:803:99//AB011148

F-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//1.2e-163:411:99//AL033531

F-HEMBA1002939//RPCI11-74014.TJ RPCI11 Homo sapiens genomic clone R-74014, genomic survey sequence.//1.7e-41:215:99//AQ266676

F-HEMBA1002944//RPCI11-55C2.TV RPCI11 Homo sapiens genomic clone R-55C2, genomic survey sequence.//1.7e-37:375:74//AQ082240

F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//0.00074:683:58//AC005578

F-HEMBA1002954//RPCI11-79F7.TV RPCI11 Homo sapiens genomic clone R-79F7, genomic survey sequence.//6.1e-24:250:78//AQ284146

F-HEMBA1002968//HS\_2262\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence.//0.99:270:60//AQ217059

F-HEMBA1002970//RPCI11-5L24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5L24, genomic survey sequence.//1.4e-10:189:71//B49289

F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 23

63L16, genomic survey sequence.//4.3e-21:181:80//AQ080538  
 F-HEMBA1002973//Rattus norvegicus Wistar 3',5'-cyclic AMP phosphodiester  
 ase (PDE4-10) gene, exon 10.//2.5e-40:257:89//U01290  
 F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone  
 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797  
 F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1  
 C) mRNA, complete cds.//3.1e-62:713:73//U20286  
 F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3  
 unordered pieces.//7.5e-50:331:85//AC005484  
 F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B  
 5, P1 clones DS02777, DS03222, DS02345, and DS04808, complete sequence./  
 /2.6e-20:357:66//AC005557  
 F-HEMBA1003034//Human DNA sequence from 4PTEL, Huntington's Disease Regi  
 on, chromosome 4p16.3.//4.5e-60:415:73//Z95704  
 F-HEMBA1003035//Homo sapiens chromosome Y, clone 264,M,20, complete sequ  
 ence.//2.3e-05:591:57//AC004617  
 F-HEMBA1003037//RPCI11-88F2.TJ RPCI11 Homo sapiens genomic clone R-88F2,  
 genomic survey sequence.//0.68:230:60//AQ286677  
 F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, comp  
 lete sequence.//8.1e-128:550:94//AC004983  
 F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-sub  
 unit mRNA, complete cds.//1.0e-164:777:98//AF054182  
 F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic  
 sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//  
 AC005505  
 F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783  
 F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complet  
 e cds.//1.5e-20:595:65//U72648  
 F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 23

66J21, genomic survey sequence.//4.4e-33:176:99//AQ080257  
 F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome  
 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuroneurin,  
 Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S rib  
 osomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, g  
 enomic marker D1S2691 and STSs.//9.4e-43:478:70//Z99297  
 F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome System  
 s Human BAC library) complete sequence.//0.96:57:85//AC004673  
 F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, com  
 plete sequence.//8.0e-74:359:81//AC004548  
 F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 com  
 plete sequence.//3.6e-11:734:58//AF001550  
 F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//I137  
 50  
 F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome regi  
 on 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308  
 F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.0005  
 4:480:60//M58564  
 F-HEMBA1003129//HS\_3139\_B2\_F05\_T7 CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey  
 sequence.//2.3e-100:510:97//AQ187635  
 F-HEMBA1003133//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequ  
 ence.//1.3e-78:370:90//AC005259  
 F-HEMBA1003136  
 F-HEMBA1003142//Homo sapiens full length insert cDNA clone ZC39B06.//6.9  
 e-121:563:100//AF086197  
 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:9  
 9//AJ005670  
 F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -

complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302  
 F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB000882

F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174:98//AL022325

F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473:59//AC005824

F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1.//1.6e-05:367:61//U09302

F-HEMBA1003202//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//9.0e-23:247:73//AC004003

F-HEMBA1003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.7e-26:141:83//Z83824

F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.9e-31:158:86//AC002037

F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.4e-24:284:75//AC004150

F-HEMBA1003222//RPCI11-47P17.TJ RPCI11 Homo sapiens genomic clone R-47P17, genomic survey sequence.//8.7e-39:202:99//AQ202885

F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone : MEB5, complete sequence.//0.86:227:62//AB019230

F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.6e-05:372:61//AE001373

F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=0, genomic survey sequence.//0.00032:57:96//B46142

F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein./  
/2.2e-08:531:59//X64624

F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6  
pA19H4.//0.070:267:64//Z78949

F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 230  
1B4, genomic survey sequence.//5.2e-08:295:63//AQ015073

F-HEMBA1003278//HS\_3075\_A1\_G09\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey  
sequence.//0.98:399:58//AQ120599

F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKI  
NG DRAFT SEQUENCE, 1 ordered pieces.//4.8e-101:277:97//AC005840

F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransfer  
ase mRNA, complete cds.//9.0e-145:539:97//AF038662

F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//5  
.0e-166:799:98//AB011109

F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2  
507M8, genomic survey sequence.//1.9e-05:388:63//AQ262551

F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met  
) gene, and partial 12S ribosomal RNA (12S rRNA) gene.//8.0e-05:388:62//  
L17343

F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence.//0  
.0017:210:64//AF051177

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, com  
plete cds.//4.6e-188:865:99//AB001872

F-HEMBA1003322//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 169I5, WORKING DRAFT SEQUENCE.//2.4e-54:316:87//Z93015

F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2  
024C24, genomic survey sequence.//8.4e-12:166:76//B67147

F-HEMBA1003328//HS\_2230\_B2\_H08\_MR CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence.//0.026:128:71//AQ153313

F-HEMBA1003330//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.0e-160:745:99//AF045555

F-HEMBA1003348//HS\_3194\_A1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence.//5.0e-79:381:99//AQ173779

F-HEMBA1003369//H.vulgare GAA-satellite DNA.//0.12:89:71//Z50100

F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence.//3.5e-32:199:80//AF024533

F-HEMBA1003373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//0.019:117:71//AL034405

F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence.//4.2e-30:196:85//U67229

F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, complete sequence.//4.6e-22:206:81//AL021528

F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00094:72:90//AC006026

F-HEMBA1003395//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00041:826:57//AL031744

F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence.//2.4e-05:265:64//AQ056234

F-HEMBA1003403//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.3e-135:780:90//AC004066

F-HEMBA1003408

F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//1.9e-41:239:95//AL031321

F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor

or (PIGR) gene, 3' UTR and trinucleotide repeat microsatellites.//2.2e-06  
:247:64//U08273

F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds.//1.4e-149:  
697:99//AF051334

F-HEMBA1003447//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete  
sequence.//1.7e-77:461:90//AC004066

F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, F  
liI (fliI) and FliJ (fliJ) genes, complete cds.//8.6e-08:752:58//U31090

F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete s  
equence.//0.089:172:68//AC004098

F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//4.5e-1  
50:562:97//AC005041

F-HEMBA1003528//Streptomyces fradiae gene for trypsinogen precursor, com  
plete cds.//4.7e-09:433:60//D16687

F-HEMBA1003531//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, compl  
ete sequence.//2.3e-48:297:90//AC004990

F-HEMBA1003538//Human complement C1r mRNA, complete cds.//4.3e-22:474:63  
//M14058

F-HEMBA1003545//Rattus norvegicus (clone 1.6kB) islet-2 mRNA, complete c  
ds.//3.5e-143:805:91//L35571

F-HEMBA1003548

F-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 447E6, WORKING DRAFT SEQUENCE.//3.4e-58:331:83//AL031724

F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome System  
s Human BAC Library) complete sequence.//6.0e-99:703:84//AC005913

F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mR  
NA, complete cds.//1.3e-99:587:89//J05071

F-HEMBA1003568//HS\_3149\_A1\_C04\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey s

equence.//4.1e-05:389:57//AQ166810  
F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.6e-102:669:85//AC005539  
F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds.//0.00033:649:58//U60170  
F-HEMBA1003579//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00034:623:56//AL031744  
F-HEMBA1003581//Mouse mRNA for talin.//3.3e-41:181:86//X56123  
F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPCI-11\_192K18 , complete sequence.//4.4e-70:273:94//AC006075  
F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence.//6.0e-17:768:58//AE001395  
F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-09:777:56//AE001398  
F-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.3e-146:692:98//AC005153  
F-HEMBA1003615//HS\_2010\_A2\_A07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence.//1.1e-22:137:97//AQ226592  
F-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//2.4e-169:501:97//AB015344  
F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds.//4.7e-37:165:92//AF034080  
F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0024:514:58//AC005139  
F-HEMBA1003630//CIT-HSP-2168N15.TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence.//6.5e-15:358:63//B92984  
F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 u



nordered pieces.//5.0e-21:238:76//AC005077  
F-HEMBA1003640//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 112K5, WORKING DRAFT SEQUENCE.//2.3e-15:371:63//Z85987  
F-HEMBA1003645//A.thaliana 81kb genomic sequence.//1.0:529:57//X98130  
F-HEMBA1003646  
F-HEMBA1003656  
F-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complet  
e sequence.//1.6e-175:824:98//AC005746  
F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE,  
21 unordered pieces.//1.1e-24:190:87//AC004765  
F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete se  
quence.//1.7e-162:579:99//AC005065  
F-HEMBA1003680//H.sapiens DNA sequence.//7.3e-22:172:87//Z22322  
F-HEMBA1003684//H.sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723  
F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds  
./2.9e-72:606:77//AF039691  
F-HEMBA1003692  
F-HEMBA1003711//Homo sapiens chromosome 17, clone HRPC41C23, complete se  
quence.//0.55:450:60//AC003101  
F-HEMBA1003714  
F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25.  
Contains STSS, GSSs and genomic marker DXS8098, complete sequence.//3.0  
e-16:316:68//AL023575  
F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, comple  
te sequence.//1.3e-41:483:73//AC004056  
F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 235  
1H9, genomic survey sequence.//1.1e-112:532:99//AQ079348  
F-HEMBA1003729//HS\_3043\_A1\_E07\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3043 Col=13 Row=I, genomic survey

sequence.//1.6e-12:87:98//AQ129345

F-HEMBA1003733//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.7e-104:761:82//AC006213

F-HEMBA1003742//HS\_3027\_A2\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731

F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey sequence.//2.9e-10:310:63//AQ113513

F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//AF060194

F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139

F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496

F-HEMBA1003784//Caenorhabditis elegans cosmid C55B6.//0.054:463:58//U88181

F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DGC R Region, complete sequence.//1.9e-44:425:76//AC000070

F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178

F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-138:275:99//AC004596

F-HEMBA1003805//Mus musculus quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940

F-HEMBA1003807//HS-1068-B1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212

F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516

F-HEMBA1003836//S.cerevisiae chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125

F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP Homo sapiens genomic clone 384 J15, genomic survey sequence.//1.4e-45:180:90//B54810

F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT987SK-1188B12 map 10 p12.1, complete sequence.//0.0014:574:58//AC005875

F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300

F-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//5.9e-81:853:71//AF030430

F-HEMBA1003879//H.sapiens CBP80 mRNA.//2.0e-08:87:95//X80030

F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.7e-180:853:98//AP000036

F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//AC004079

F-HEMBA1003893//H.sapiens CpG island DNA genomic MseI fragment, clone 11 b6, forward read cpg11b6.ft1a.//3.6e-32:173:99//Z59012

F-HEMBA1003902//RPCI11-26M20.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-26M20, genomic survey sequence.//8.2e-12:422:61//AQ003455

F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.0063:468:58//AE001401

F-HEMBA1003926//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310013, WORKING DRAFT SEQUENCE.//3.6e-27:278:76//AL031658

F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//1.4e-55:315:81//AF109718

F-HEMBA1003939//HS-1047-A1-G04-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=7 Row=M, genomic survey sequence.//6.1e-09:413:63//B38195

F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.42:205:65//AC005140

F-HEMBA1003950//M.capricolum DNA for CONTIG MC072.//0.029:458:58//Z33058

F-HEMBA1003953//HS\_2268\_A1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=7 Row=C, genomic survey sequence.//9.0e-07:239:64//AQ085098

F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.8e-57:424:74//AC004894

F-HEMBA1003959//RPCI11-78E8.TV RPCI11 Homo sapiens genomic clone R-78E8, genomic survey sequence.//4.3e-86:441:96//AQ285498

F-HEMBA1003976//HS\_3146\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=17 Row=0, genomic survey sequence.//6.3e-10:129:80//AQ141146

F-HEMBA1003978

F-HEMBA1003985//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y105C5, WORKING DRAFT SEQUENCE.//1.0:258:60//Z98855

F-HEMBA1003987

F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9.//0.40:238:61//AL034446

F-HEMBA1004000//Rattus norvegicus satellite sequence d0Mco2.//2.0e-07:116:70//U19354

F-HEMBA1004011//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.098:286:60//AC004710

F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//2.8e-185:896:97//AC005670

F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence.//6.3e-68:417:80//AC005411

F-HEMBA1004024//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.0e-47:418:77//AC005859

F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28, WORKING DRAFT SEQUENCE.//1.6e-51:564:74//AP000052

F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.2e-05:636:55//AE001398

F-HEMBA1004045//Homo sapiens (subclone 1\_g7 from BAC H76) DNA sequence, complete sequence.//1.9e-31:373:76//AC002252

F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2.//0.039:234:63//D63393

F-HEMBA1004049//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//4.8e-135:780:89//AC003106

F-HEMBA1004055//Human chromosome 3p21.1 gene sequence.//4.7e-09:457:58//L13435

F-HEMBA1004056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//3.3e-25:246:77//AL021977

F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey sequence.//7.8e-24:233:76//B68555

F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Varlp (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//4.5e-08:614:59//U49822

F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//5.9e-121:502:85//AF091234

F-HEMBA1004111//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.0e-36:317:80//AC006160

F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence.//8.7e-24:320:71//AF046393

F-HEMBA1004132//HS\_3226\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=3226 Col=19 Row=H, genomic survey sequence.//9.7e-13:232:71//AQ182017

F-HEMBA1004133

F-HEMBA1004138//HS\_3036\_B1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=N, genomic survey sequence.//0.0035:165:64//AQ294763

F-HEMBA1004143

F-HEMBA1004146

F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.00011:618:60//Z96811

F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//2.9e-30:454:68//AC005913

F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855

F-HEMBA1004199

F-HEMBA1004200//HS\_2015\_A1\_B05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957

F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268\_P\_23, complete sequence.//7.8e-59:216:83//AC004807

F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//6.3e-98:173:98//AC005488

F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748

F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424

F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927

F-HEMBA1004238

F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708

F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24. 1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//AL031010

F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6) mRNA, complete cds.//1.7e-30:315:74//L13619

F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//AC004693

F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//3.1e-78:335:87//AC004707

F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831

F-HEMBA1004274//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993

F-HEMBA1004275//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051

F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477

F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:99//AF022795

F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MQN23, complete sequence.//1.0:387:59//AB013395

F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-06:92:89//AB012254

F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897

F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome;  
segment 2/4.//0.28:522:57//AJ235271

F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete se  
quence.//7.1e-136:548:92//AC006130

F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3  
e-32:320:65//Z84720

F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.  
93:222:62//AB011094

F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//7.0e-168:895:93//AC004995

F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library  
) complete sequence.//4.6e-73:713:75//AC002980

F-HEMBA1004335//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL024498

F-HEMBA1004341

F-HEMBA1004353//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequenc  
e.//6.4e-38:278:85//U14571

F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively  
spliced, complete cds.//4.1e-45:190:92//U75968

F-HEMBA1004356

F-HEMBA1004366//P.falciparum complete gene map of plastid-like DNA (IR-A  
) .//2.2e-07:736:57//X95275

F-HEMBA1004372//H.sapiens dystrophin gene intron 44.//1.0:129:62//X77644

F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//  
4.7e-42:237:94//M21977

F-HEMBA1004394//Plasmodium falciparum chromosome 2, section 39 of 73 of  
the complete sequence.//5.2e-05:519:59//AE001402

F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence.//  
4.0e-32:261:76//AC002463



F-HEMBA1004405//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.4e-07:693:58//AC005507

F-HEMBA1004408//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-69:195:100//AC005037

F-HEMBA1004429//HS\_3193\_A1\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3193 Col=11 Row=C, genomic survey sequence.//5.1e-67:386:91//AQ172942

F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//3.2e-27:242:82//AC002554

F-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.7e-75:590:81//AC004846

F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, complete sequence.//0.045:215:66//AL034407

F-HEMBA1004479//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//5.2e-43:364:79//AF060194

F-HEMBA1004482//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//6.8e-17:791:59//AC005505

F-HEMBA1004499//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//4.4e-125:251:94//AC004686

F-HEMBA1004502//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.012:635:57//AC004709

F-HEMBA1004506//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.8e-127:766:88//AC004453

F-HEMBA1004507

F-HEMBA1004509//Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project).//1.0e-13:244:67//AL021712

F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280)  
 .//1.6e-72:678:74//X53416

F-HEMBA1004538//Sequence 1 from patent US 5612190.//0.00015:416:59//I368  
 71

F-HEMBA1004542//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5  
 unordered pieces.//0.95:202:64//AC005038

F-HEMBA1004554//Arabidopsis thaliana BAC T26D22.//0.45:624:56//AF058826

F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//9.1e-10:173  
 :70//D87457

F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence.//  
 6.1e-23:134:73//AC002542

F-HEMBA1004577//Homo sapiens Chromosome 16 BAC clone CIT987SK-582J2, com  
 plete sequence.//1.6e-15:190:77//AC004525

F-HEMBA1004586//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8  
 unordered pieces.//3.1e-31:388:76//AC004895

F-HEMBA1004596//RPCI11-81021.TJ RPCI11 Homo sapiens genomic clone R-8102  
 1, genomic survey sequence.//2.2e-90:458:90//AQ285136

F-HEMBA1004604//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, comp  
 lete cds.//8.6e-105:699:84//AF071316

F-HEMBA1004610//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, comp  
 lete sequence.//5.4e-20:267:72//AC004983

F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP Homo sapiens genomic clone 23  
 19H15, genomic survey sequence.//6.2e-26:147:99//AQ034944

F-HEMBA1004629//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomi  
 c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.6e-06:766:56/  
 /AC005504

F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Conta  
 ins ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STS  
 s.//4.7e-73:412:92//Z83843

F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EH V1 ORF 46, VZV ORF 44.//0.92:181:61//X90418

F-HEMBA1004637//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//7 .8e-47:784:65//X74904

F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds.//6.4e-06:458:61//AF004431

F-HEMBA1004666//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.30:733:55//Z98865

F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//7.5e-136:521:98//AL031432

F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence.//0.43:365:59//AC000045

F-HEMBA1004672

F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.096:651:54//AC 005308

F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 23 26C13, genomic survey sequence.//0.23:238:65//AQ040642

F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//2.1e-27:375:72//AC002357

F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.6e-36:191:91//AC006210

F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//1.1e-133:639:99//AC005562

F-HEMBA1004725//RPCI11-75013.TJ RPCI11 Homo sapiens genomic clone R-7501 3, genomic survey sequence.//6.2e-32:169:100//AQ266512

F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence.//

8.0e-68:732:72//AC004029

F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 23  
05M23, genomic survey sequence.//4.9e-18:209:69//AQ017556

F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UB  
C17) mRNA, complete cds.//1.8e-13:451:62//AF028340

F-HEMBA1004736//Human DNA sequence from PAC 436M11 on chromosome Xp22.11  
-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and  
the first coding exon of the RSI gene for retinoschisis (X-linked, juve  
nile) 1 (XLRSl). Contains ESTs, an STS and GSSs, complete sequence.//5.0  
e-87:646:78//Z94056

F-HEMBA1004748//Human BAC clone RG204I16 from 7q31, complete sequence.//  
0.24:526:57//AC002461

F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//1.4e-25:268:76//AC004913

F-HEMBA1004752//R.norvegicus mRNA for leucocyte common antigen-related p  
rotein (3941 bp).//1.1e-07:503:61//X83546

F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete se  
quence.//4.5e-38:314:81//AC000028

F-HEMBA1004756//Homo sapiens, complete sequence.//1.4e-111:326:84//AC005  
854

F-HEMBA1004758//Sequence 29 from patent US 5534410.//3.9e-135:769:91//I2  
3472

F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete  
cds.//3.6e-47:404:79//U75285

F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete  
sequence.//6.7e-107:890:78//AC004941

F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomi  
c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-09:806:59/  
/AC004709

F-HEMBA1004771//G.muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA.//0.69:239:61//X65063

F-HEMBA1004776

F-HEMBA1004778

F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550 mRNA, partial cds.//3.4e-46:778:64//AF003622

F-HEMBA1004803//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.3e-82:580:82//AC004617

F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//5.4e-07:642:59//AC005083

F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3.//1.4e-46:171:92//L01042

F-HEMBA1004816//Homo sapiens calpastatin (CAST) gene, exons 10-14.//3.5e-31:546:66//M86257

F-HEMBA1004820//C.botulinum progenitor toxin complex genes.//0.0014:343:62//X87972

F-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//1.5e-85:512:88//X53744

F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFBRI) gene, exon 1.//0.0065:284:61//AF054590

F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence.//0.92:250:59//AC000400

F-HEMBA1004864

F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//3.6e-12:214:72//AL031120

F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.1e-08:255:69//AC004020

F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (An

tp) mRNA, complete cds.//0.062:155:69//U32943  
 F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence.//0.000  
 55:323:60//L12043  
 F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequen  
 ce.//9.6e-16:166:80//AC003051  
 F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene  
 , partial.//0.81:146:65//M94003  
 F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmid  
 s R32543, , and F15613 containing ZNF gene family member, genomic sequen  
 ce, complete sequence.//1.4e-36:338:78//AC003006  
 F-HEMBA1004929//CIT-HSP-2373I16.TR CIT-HSP Homo sapiens genomic clone 23  
 73I16, genomic survey sequence.//2.4e-86:443:96//AQ108676  
 F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete seq  
 uence.//4.6e-20:219:73//AC004109  
 F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C  
 Homo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey seq  
 uence.//1.4e-28:216:85//B30726  
 F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267010, complete seq  
 uence.//0.53:222:61//AF042091  
 F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5  
 unordered pieces.//1.2e-58:509:78//AC005482  
 F-HEMBA1004954//HS\_2033\_A2\_A08\_T7 CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey  
 sequence.//3.7e-47:243:99//AQ229758  
 F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B  
 ).//0.048:421:58//X95276  
 F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fra  
 gment No. 8.//0.89:333:58//Z97343  
 F-HEMBA1004972

F-HEMBA1004973//RPCI11-66P8.TK RPCI11 Homo sapiens genomic clone R-66P8,  
genomic survey sequence.//3.5e-22:245:77//AQ238471

F-HEMBA1004977//Homo sapiens full length insert cDNA clone YZ83B08.//9.0  
e-11:84:98//AF086080

F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 23  
54E10, genomic survey sequence.//0.0021:152:66//AQ075713

F-HEMBA1004980//HS\_3018\_A2\_E04\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey s  
equence.//1.9e-77:392:97//AQ071873

F-HEMBA1004983//Albinaria corrugata isolate cor.Prnl.1 16S ribosomal RNA  
gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.00  
30:276:61//AF031680

F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (L  
ANL), complete sequence.//4.2e-138:640:99//AC005590

F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequ  
ence.//6.8e-20:160:88//U52077

F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//2.0e-1  
44:668:99//AF041474

F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//1.  
4e-146:693:98//AB014548

F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6  
p21.3-22.2: Contains an unknown pseudogene, a 60S Ribosomal protein L24  
(L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseud  
ogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA  
-Thr gene. Contains ESTs, STSSs, GSSs and genomic marker D6S464, complete  
sequence.//2.2e-115:668:90//AL009179

F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete  
sequence.//4.6e-138:591:98//AC004596

F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 233

8L5, genomic survey sequence.//3.7e-61:271:88//AQ055486

F-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//3.8e-17:218:73//Z2  
2819

F-HEMBA1005050//Human Tis11d gene, complete cds.//0.079:251:63//U07802

F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic  
sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.018:560:56//AC0  
04688

F-HEMBA1005066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 774G10, WORKING DRAFT SEQUENCE.//3.4e-97:432:84//AL034410

F-HEMBA1005075//H.sapiens DNA 3' flanking simple sequence region clone w  
g2c3.//6.9e-07:176:68//X76589

F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2.  
325M21, genomic survey sequence.//2.1e-48:274:93//AQ038720

F-HEMBA1005083//HS\_2248\_B1\_D05\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey s  
equence.//3.4e-06:230:64//AQ129575

F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete  
cds.//1.3e-161:762:98//AF080561

F-HEMBA1005113//L.esculentum microsatellite repeat DNA region.//0.0038:7  
42:57//X90770

F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33  
unordered pieces.//9.6e-83:479:78//AC004854

F-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone Y313F4, WORKING DRAFT SEQUENCE.//3.9e-24:576:64//AL023808

F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, compl  
ete sequence.//4.7e-36:283:80//AC004542

F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUEN  
CE, 99 unordered pieces.//5.0e-10:332:64//AC004469

F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/



5, WORKING DRAFT SEQUENCE.//4.0e-10:734:58//AP000023  
 F-HEMBA1005185//H.sapiens CpG island DNA genomic MseI fragment, clone 91  
 b2, forward read cpg91b2.ft1a.//2.2e-14:93:100//Z63847  
 F-HEMBA1005201//Drosophila melanogaster cosmid 152A3.//4.7e-35:679:64//A  
 L009194  
 F-HEMBA1005202//Canine mRNA for 68kDA subunit of signal recognition part  
 icle (SRP68).//6.7e-138:778:90//X53744  
 F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and pa  
 rtial o25 gene and Pros26 gene.//7.1e-12:376:62//AJ011320  
 F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds.//7  
 .1e-05:411:60//AB007914  
 F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, compl  
 ete sequence.//3.5e-06:212:66//AC004542  
 F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic  
 sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-07:625:57//  
 AC005308  
 F-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete  
 sequence.//8.7e-45:567:72//AC005154  
 F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5,  
 174A6, U172D6, and U186B3 from Xp22, complete sequence.//0.96:298:62//AC  
 002365  
 F-HEMBA1005251  
 F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complet  
 e sequence.//4.5e-160:392:99//AC005837  
 F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 g  
 ene, complete sequence.//2.3e-05:496:60//AF069291  
 F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3  
 -23. Contains an EST, an STS and GSSs, complete sequence.//5.7e-05:220:6  
 4//AL033521

F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//2.4e-20:338:65//U97018

F-HEMBA1005296

F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//1.6e-51:381:78//AL031012

F-HEMBA1005311

F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//0.94:226:63//AP000031

F-HEMBA1005315//Homo sapiens BAC810, complete sequence.//9.5e-15:684:62//U85198

F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone.//2.6e-05:472:59//Z83823

F-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//3.3e-90:300:90//AC005803

F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//1.4e-151:740:97//AJ007581

F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey sequence.//2.1e-86:438:97//AQ016145

F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds.//1.8e-98:500:88//U09414

F-HEMBA1005367//Mus musculus melastatin mRNA, complete cds.//8.3e-72:577:73//AF047714

F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS.//1.3e-07:274:66//Z82900

F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.9e-48:611:69//AC004813

F-HEMBA1005382//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey

sequence.//1.6e-27:154:98//AQ103204

F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence.//4.0e-07:443:61//M23175

F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey sequence.//7.6e-17:225:71//AQ076749

F-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//4.5e-131:278:98//AL034379

F-HEMBA1005408//HS\_3007\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=8 Row=N, genomic survey sequence.//8.0e-06:218:66//AQ294366

F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocerebrorenal syndrome (OCRL) ESTs and STS.//1.5e-41:432:76//Z73496

F-HEMBA1005411

F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//1.0e-169:537:99//AF041248

F-HEMBA1005426

F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-37:260:76//AC006130

F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey sequence.//5.0e-133:631:98//B93234

F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.5e-118:868:83//AL022576

F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//1.2e-179:838:99//AC005212

F-HEMBA1005472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//3.4e-20:187:74//AL031985

F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12 /28, WORKING DRAFT SEQUENCE.//4.1e-22:445:65//AP000041

F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sapiens genomic clone 23 22D14, genomic survey sequence.//6.7e-51:269:97//AQ026941

F-HEMBA1005497//HS\_3097\_A2\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3097 Col=10 Row=M, genomic survey sequence.//1.4e-66:345:96//AQ103810

F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence.//5.4e-178:818:98//AC004957

F-HEMBA1005506//Mus musculus (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds.//2.6e-06:73:98//L12147

F-HEMBA1005508//Homo sapiens, clone hRPK.1\_A\_1, complete sequence.//0.00 012:455:60//AC006196

F-HEMBA1005511//Homo sapiens MHC class 1 region.//3.3e-43:421:77//AF0550 66

F-HEMBA1005513//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//2.3e-20:352:69//U71219

F-HEMBA1005517//Homo sapiens DNA for (CGG)<sub>n</sub> trinucleotide repeat region, isolate E7.//2.5e-08:431:62//AJ001216

F-HEMBA1005518//M.musculus mRNA for paladin gene.//8.2e-90:651:81//X9938 4

F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.8e-167:755:99//AC004913

F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//2.4e-42:475:73//AC006241

F-HEMBA1005528//Mus musculus mCAF1 protein mRNA, complete cds.//1.2e-94: 512:92//U21855

F-HEMBA1005530

F-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 970A17, WORKING DRAFT SEQUENCE.//9.4e-87:422:99//AL034431

F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//AC004743

F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377

F-HEMBA1005568//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153

F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407

F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932

F-HEMBA1005577//HS-1004-A1-E11-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971

F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531

F-HEMBA1005582//HS\_3242\_A1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275

F-HEMBA1005583

F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025

F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.3e-158:748:99//AC005746

F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527

F-HEMBA1005606//CIT-HSP-2326I6.TR CIT-HSP Homo sapiens genomic clone 2326I6, genomic survey sequence.//0.0014:132:70//AQ041484

F-HEMBA1005609//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:85//AC005089

F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome X q21.1-Xq21.3. rab proteins geranylgeranyltransferase component A 1 (rab escort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//6.5e-29:279:69//AL009175

F-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731

F-HEMBA1005627//RPCI11-34P9.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34P9, genomic survey sequence.//0.014:168:67//AQ045110

F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004460

F-HEMBA1005632

F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33. Contains ESTs.//6.6e-38:452:67//Z98036

F-HEMBA1005666

F-HEMBA1005670//Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.//5.1e-59:687:74//AC004850

F-HEMBA1005679//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-47:357:85//AC005478

F-HEMBA1005680

F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742

F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-72:406:92//U57001

F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513

F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348

F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697

F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.//5.6e-15:157:79//AC005156

F-HEMBA1005746//RPCI11-63N8.TK RPCI11 Homo sapiens genomic clone R-63N8, genomic survey sequence.//1.3e-18:113:100//AQ238535

F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome X p11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.6e-56:764:70//Z97181

F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qter contains ESTs and polymorphic CA repeat (D22S1152).//1.1e-30:275:77//Z82196

F-HEMBA1005780//RPCI11-74E19.TJ RPCI11 Homo sapiens genomic clone R-74E19, genomic survey sequence.//0.0011:283:62//AQ268432

F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//0.14:326:61//AC004079

F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:59//X92523

F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.87:417:56//AC003020

F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DGCR Region, complete sequence.//8.8e-42:370:79//AC000094

F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577

F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey sequence.//4.3e-07:253:59//AL018749

F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone 2289L23, genomic survey sequence.//2.2e-68:333:99//B98952

F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), complete sequence.//1.9e-57:331:87//AC005351

F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//5.1e-182:864:98//AC004945

F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//3.0e-44:340:80//AC004086

F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1 q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026

F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584

F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.3e-41:431:77//AC005666

F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPCI4-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086

F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974

F-HEMBA1005962//RPCI11-17015.TV RPCI-11 Homo sapiens genomic clone RPCI-11-17015, genomic survey sequence.//9.5e-36:315:84//B82821

F-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=1, genomic survey sequence.//9.3e-73:372:97//AQ147357



F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516

F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:423:60//AE001408

F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599

F-HEMBA1006002

F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405

F-HEMBA1006031

F-HEMBA1006035

F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:74//D87009

F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10 q25, complete sequence.//2.1e-43:330:70//AC005386

F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153

F-HEMBA1006081

F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500

F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098

F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10 q25, complete sequence.//2.8e-18:180:78//AC005880

F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains

ESTs, STSS, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177

F-HEMBA1006121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672

F-HEMBA1006124//CIT-HSP-2355B17.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966

F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085

F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome X q25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSS and GSSs, complete sequence.//7.5e-22:164:75//AL022162

F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500

F-HEMBA1006155//H.sapiens CpG island DNA genomic MseI fragment, clone 119b6, forward read cpg119b6.ft1a.//1.0:85:72//Z64428

F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185:852:99//AF048693

F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].//8.4e-50:642:73//S49400

F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ105i19, complete sequence.//1.4e-22:194:74//AC005318

F-HEMBA1006198

F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557

F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074

F-HEMBA1006252//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664

F-HEMBA1006253

F-HEMBA1006259//HS\_2231\_A1\_D10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722

F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673

F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791

F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//2.1e-57:665:70//U58134

F-HEMBA1006283

F-HEMBA1006284//Streptomyces fradiae tyllactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//9.6e-06:623:60//U78289

F-HEMBA1006291//HS\_2208\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804

F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415

F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070

F-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183

F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074

F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563

F-HEMBA1006344//HS-1009-A2-B02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420

F-HEMBA1006347//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//1.6e-31:484:68//U71219

F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671

F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244

F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413

F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence.//3.0e-57:401:81//AC002327

F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP Homo sapiens genomic clone 2172K18, genomic survey sequence.//1.3e-110:525:99//B92570

F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 828 Col=20 Row=L, genomic survey sequence.//4.4e-05:163:70//B37813

F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.8e-62:370:86//AC004806

F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//3.7e-15:157:78//AC005179

F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//1.2e-39:752:63//AL022165

F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown g

enes.//2.4e-41:438:76//AF107885

F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//0.027:293:64//AL031781

F-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//1.7e-50:310:80//Z93930

F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA./0.051:440:59//X04465

F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds.//1.0:238:59//U62088

F-HEMBA1006446//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//2.4e-05:702:58//AL031749

F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//8.6e-55:409:83//AC004560

F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.0:293:59//AC006120

F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.4e-05:731:59//AC004709

F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence.//5.2e-60:435:83//B54247

F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence.//2.9e-48:286:84//AC004752

F-HEMBA1006485//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.96:283:59//AC006031

F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related

, matrix associated, actin dependent regulator of chromatin, subfamily a  
 , member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains  
 ESTs, STSs and GSSs, complete sequence.//1.8e-14:259:67//AL022577  
 F-HEMBA1006489//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 467K16, WORKING DRAFT SEQUENCE.//6.6e-11:595:61//AL031283  
 F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complet  
 e sequence.//6.0e-122:337:100//AC005828  
 F-HEMBA1006494//Homo sapiens chromosome 7qtelo BAC E3, complete sequence  
 .//3.8e-23:459:68//AF093117  
 F-HEMBA1006497//HS\_3023\_B2\_H03\_T7 CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey s  
 equence.//2.3e-81:433:95//AQ093846  
 F-HEMBA1006502//H.sapiens 7SL repeat (clones 2-19b).//1.6e-13:86:87//X62  
 364  
 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//2.  
 3e-139:470:98//AB014566  
 F-HEMBA1006521//Human BAC clone RG167B05 from 7q21, complete sequence.//  
 4.3e-27:406:71//AC003991  
 F-HEMBA1006530//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 1018D12, WORKING DRAFT SEQUENCE.//2.9e-27:408:65//AL031650  
 F-HEMBA1006535//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from MAL4P1, WORKING DRAFT SEQUENCE.//0.028:599:60//AL034557  
 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA  
 , complete cds.//1.4e-171:654:98//AF093419  
 F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers D  
 XS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene  
 .//3.8e-104:811:80//Z73986  
 F-HEMBA1006559//Mus musculus PRAJA1 (Praj1) mRNA, complete cds.//4.8e-9  
 9:386:82//U06944

F-HEMBA1006562//Human fructose-1,6-biphosphatase (FBP1) gene, exon 1.//0.012:322:60//U21925

F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0026:580:58//AC005504

F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//6.3e-08:231:70//U39357

F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone 2380A22, genomic survey sequence.//0.036:250:62//AQ197107

F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.0:225:63//AL021841

F-HEMBA1006595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156

F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-42:253:84//AC004166

F-HEMBA1006612//RPCI11-88F20.TJ RPCI11 Homo sapiens genomic clone R-88F20, genomic survey sequence.//1.1e-51:266:98//AQ286726

F-HEMBA1006617//HS\_2193\_B2\_H07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence.//1.1e-59:413:85//AQ299685

F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//1.4e-35:257:89//AL023284

F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//9.6e-112:800:83//AC002036

F-HEMBA1006635//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*

from MAL1P2, WORKING DRAFT SEQUENCE.//0.15:393:58//AL031745  
 F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP)  
 mRNA, complete cds.//9.6e-15:318:68//AF032896  
 F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1  
 unordered pieces.//0.58:254:65//AC006148  
 F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, compl  
 ete cds.//1.5e-37:108:88//U94479  
 F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180),  
 complete sequence.//1.3e-154:671:96//AC005601  
 F-HEMBA1006653  
 F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete  
 sequence.//5.2e-110:254:93//AC005189  
 F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human B  
 AC library) complete sequence.//1.4e-14:177:76//AC004554  
 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56.//5.5e-15  
 :122:90//Y12065  
 F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete seque  
 nce.//0.098:218:63//AC004755  
 F-HEMBA1006682//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 668J24, WORKING DRAFT SEQUENCE.//1.4e-05:719:57//AL034346  
 F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence.//3.1e-2  
 2:151:78//AC006011  
 F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone  
 2522D16, genomic survey sequence.//5.6e-17:324:66//AQ280738  
 F-HEMBA1006708  
 F-HEMBA1006709  
 F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 u  
 nordered pieces.//3.3e-08:136:79//AC005537  
 F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complet



e sequence.//5.8e-162:497:98//AC005828

F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//7.4e-48:320:87//AC004796

F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs.//4.1e-129:804:85//Z83850

F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//2.2e-162:766:99//AC005752

F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence.//1.2e-19:326:69//U73465

F-HEMBA1006779//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//1.4e-103:355:87//AL022727

F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 2359P7, genomic survey sequence.//0.072:147:68//AQ077208

F-HEMBA1006789//nbxb0037I13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037I13r, genomic survey sequence.//0.00011:288:63//AQ290474

F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 2307E3, genomic survey sequence.//5.1e-80:420:96//AQ020511

F-HEMBA1006796//Human clone 23803 mRNA, partial cds.//4.5e-06:202:68//U79298

F-HEMBA1006807//Homo sapiens mRNA for SPOP.//1.2e-66:651:73//AJ000644

F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_0\_9, complete sequence.//6.0e-116:541:99//AC004797

F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//0.40:159:66//AC004262

F-HEMBA1006832//Homo sapiens (subclone 3\_g8 from P1 H25) DNA sequence, complete sequence.//1.8e-24:323:71//AC002196

F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat e  
pithelium cancer , segment 4/10.//0.15:403:60//AB020872

F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of t  
he complete sequence.//0.20:472:57//AE001369

F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence.//3.  
4e-79:641:76//AF046757

F-HEMBA1006885//HS\_2208\_B2\_G06\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey  
sequence.//4.9e-18:206:76//AQ089246

F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.  
2-12.3 Contains EST, GSS, complete sequence.//5.4e-07:298:65//AL031321

F-HEMBA1006914//S.pombe chromosome II cosmid c16H5.//0.00040:194:66//AL0  
22104

F-HEMBA1006921//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete  
sequence.//1.1e-174:813:99//AC006027

F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185.//0.0075:183:65//AF0  
36704

F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A  
) .//4.0e-06:739:57//X95275

F-HEMBA1006936

F-HEMBA1006938//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL1P4, WORKING DRAFT SEQUENCE.//1.1e-05:733:57//AL031747

F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.  
//1.3e-90:437:98//AJ010841

F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X. conta  
ins STS and polymorphic CA repeat.//0.67:217:62//Z82205

F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete c  
ds.//5.6e-143:740:94//AF004828

F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase.//2.8e-101:

338:89//E06058

F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//7.1e-31:536:66//AC003071

F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//9.5e-07:285:60//Z82209

F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence.//0.99:388:58//AC002328

F-HEMBA1007017//Sequence 3 from Patent W09416067.//0.96:220:62//A39358

F-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//1.3e-124:838:83//X79088

F-HEMBA1007045

F-HEMBA1007051//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.17:343:60//Z99281

F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.3e-67:659:74//U85056

F-HEMBA1007062//Tubulin gene.//1.0:113:67//A18572

F-HEMBA1007066//HS\_3116\_A2\_A03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence.//0.80:214:62//AQ140467

F-HEMBA1007073//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.3e-54:519:68//AC004242

F-HEMBA1007078//CIT-HSP-2318N6.TF CIT-HSP Homo sapiens genomic clone 2318N6, genomic survey sequence.//8.7e-80:387:98//AQ044076

F-HEMBA1007080

F-HEMBA1007085//Streptomyces coelicolor cosmid 7A1.//3.5e-06:496:59//AL034447

F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence.//7.4e-07:553:56//Z98551

F-HEMBA1007112//HS\_2171\_A1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence.//1.0:172:61//AQ091865

F-HEMBA1007113//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//0.54:502:56//AL023875

F-HEMBA1007121//Caenorhabditis elegans cosmid ZK430.//1.4e-08:265:64//U42833

F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 Homo sapiens genomic clone 2504A5, genomic survey sequence.//0.97:267:62//AQ264035

F-HEMBA1007147//HS\_3208\_A2\_C04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence.//9.1e-90:466:95//AQ176696

F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//6.0e-138:524:98//AC005239

F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//2.0e-20:157:87//AQ280780

F-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds.//2.0e-62:318:97//AF062085

F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC111-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//1.6e-21:205:80//AC005911

F-HEMBA1007194//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.3e-11:87:96//AQ187492

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.7e-156:478:98//D86987

F-HEMBA1007206//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.024:342:63//AC004223

F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//5.0e-176:839:98//AB018340

F-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//4.3e-58:687:68  
//J00060

F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129).//0.  
084:177:62//V00899

F-HEMBA1007256//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 328E19, WORKING DRAFT SEQUENCE.//1.3e-75:490:88//AL022240

F-HEMBA1007267//HS\_3218\_A1\_F07\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey  
sequence.//2.9e-62:393:87//AQ181128

F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 21  
71B10, genomic survey sequence.//1.1e-63:314:99//B95401

F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10,  
complete sequence.//3.1e-31:401:72//AC004638

F-HEMBA1007281//HS\_3115\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey  
sequence.//5.0e-70:372:96//AQ186691

F-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24  
Contains EST, STS, GSS, CpG island, complete sequence.//1.2e-152:727:98/  
/AL031003

F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3',5'-Cyclic GMP Phosphod  
iesterase, complete cds.//2.1e-21:542:63//AB008467

F-HEMBA1007301//COL1A1=type I collagen pro alpha 1(I) chain propeptide {  
3' region} [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Muta  
nt, 855 nt].//1.7e-08:388:61//S64596

F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence.//6.0e-  
84:390:75//AC000399

F-HEMBA1007320

F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete  
sequence.//0.091:260:64//AC004485

F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.12:472:59//AC005140

F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.5e-18:408:64//AC006120

F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//8.7e-25:500:62//AC005377

F-HEMBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete sequence.//0.75:269:61//AC005738

F-HEMBB1000005//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//5.0e-05:441:60//AC004617

F-HEMBB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491

F-HEMBB1000018//HS\_2179\_B2\_E04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250

F-HEMBB1000024//Human DNA sequence from PAC 106I20 on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS.//8.1e-11:461:61//Z81369

F-HEMBB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.96:198:62//AQ062938

F-HEMBB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173

F-HEMBB1000036//H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857

F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928

F-HEMBB1000039//HS\_2167\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey

sequence.//0.022:108:69//AQ092404

F-HEMBB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome.//1.0e-07:486:61//AE001164

F-HEMBB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507

F-HEMBB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene. Contains ESTs, STSS and GSSs, complete sequence.//5.8e-38:549:67//AL022170

F-HEMBB1000054//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349

F-HEMBB1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE.//3.7e-05:600:58//AB000880

F-HEMBB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096

F-HEMBB1000083

F-HEMBB1000089//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.0036:679:56//AL031744

F-HEMBB1000099//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909

F-HEMBB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210

F-HEMBB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450

F-HEM BB1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521  
F-HEM BB1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.//0.59:217:66//Z74697  
F-HEM BB1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090  
F-HEM BB1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542  
F-HEM BB1000173//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//9.4e-160:562:93//AC002996  
F-HEM BB1000175  
F-HEM BB1000198//HS\_3071\_A2\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388  
F-HEM BB1000215//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete sequence.//6.7e-17:138:86//AC005839  
F-HEM BB1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808  
F-HEM BB1000218//Caenorhabditis elegans cosmid C52A11, complete sequence.//0.90:337:56//Z46792  
F-HEM BB1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.7e-90:175:92//Z69890  
F-HEM BB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence.//0.16:171:62//U07918  
F-HEM BB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.8e-08:355:63//AC005522  
F-HEM BB1000250//Homo sapiens protein associated with Myc mRNA, complete



cds.//6.6e-155:735:98//AF075587  
 F-HEMBB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16.//0.58:396:59//M98818  
 F-HEMBB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.4e-32:100:100//U75968  
 F-HEMBB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.8e-16:176:78//AC004470  
 F-HEMBB1000272//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.011:379:58//AE001369  
 F-HEMBB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project).//0.92:272:61//AL022580  
 F-HEMBB1000284//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//0.00071:568:57//AC002366  
 F-HEMBB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like; zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene.//3.0e-13:439:65//Z98745  
 F-HEMBB1000312//Homo sapiens clone GS051M12, complete sequence.//0.031:252:65//AC005007  
 F-HEMBB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence.//0.00033:173:65//AL026242  
 F-HEMBB1000318//HS\_3244\_B2\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence.//3.9e-85:438:95//AQ252951  
 F-HEMBB1000335//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence.//0.63:285:61//AC005968  
 F-HEMBB1000336  
 F-HEMBB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence.//0.0014:309:64//AC004051

F-HEMBB1000338//HS\_3108\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence.//3.8e-09:331:63//AQ140356

F-HEMBB1000339//Homo sapiens 12q24 PAC RPCI1-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-52:295:77//AC002351

F-HEMBB1000341

F-HEMBB1000343//Plasmodium falciparum MAL3P3, complete sequence.//0.00081:397:61//Z98547

F-HEMBB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//9.1e-34:596:66//AL020989

F-HEMBB1000369//Genomic sequence from Human 17, complete sequence.//0.012:298:60//AC002090

F-HEMBB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//9.3e-69:294:89//U96409

F-HEMBB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSS and GSSs, complete sequence.//3.5e-54:352:88//AL034377

F-HEMBB1000391//Trichothecium roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.//0.011:168:67//U51982

F-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//2.6e-163:762:98//AF076838

F-HEMBB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing MR2 gene exons 1,2, and 3, complete sequence.//7.7e-15:466:63//AC002368

F-HEMBB1000404//Homo sapiens mRNA for myosin-IXA.//3.5e-65:324:98//AJ001714

F-HEMBB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D11S1

through D11S25, complete sequence.//0.013:399:62//AC001228

F-HEM BB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//6.1e-83:571:84//AC004263

F-HEM BB1000438//RPCI11-21E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21E14, genomic survey sequence.//0.0030:295:63//B83110

F-HEM BB1000441//Homo sapiens Chromosome 22q12 Cosmid Clone 1147g11, complete sequence.//2.5e-33:372:72//AC000035

F-HEM BB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//1.3e-51:534:72//Z83821

F-HEM BB1000455//Saccharomyces cerevisiae mitochondrion origin of replication (ori6) and oli1 gene, complete cds.//0.016:522:58//L36899

F-HEM BB1000472

F-HEM BB1000480

F-HEM BB1000487//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 12803, WORKING DRAFT SEQUENCE.//0.00013:314:64//Z98742

F-HEM BB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//4.1e-110:529:98//AL034423

F-HEM BB1000491//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.10:187:65//AE001388

F-HEM BB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-06:637:58//AL022577

F-HEM BB1000510//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//3.1e-96:737:81//AC005553

F-HEMBB1000518//Homo Sapiens Chromosome X clone bWxD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.00014:163:68//AC004676

F-HEMBB1000523//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.41:349:56//AL010212

F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.//6.6e-37:138:96//Y11710

F-HEMBB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11. //3.9e-56:683:71//AB020860

F-HEMBB1000554//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//2.2e-51:282:84//AJ011929

F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds.//6.1e-32:537:65//AB018293

F-HEMBB1000564

F-HEMBB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.2e-33:268:73//AC005077

F-HEMBB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTS, STSSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//5.8e-47:734:66//AL022476

F-HEMBB1000586//H.sapiens highly polymorphic microsatellite DNA.//0.030:147:67//X79883

F-HEMBB1000589//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.3e-41:278:83//AC002300

F-HEMBB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.1e-182:871:98//AC005184

F-HEMBB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region,

partial sequence. clone #19.//0.012:185:64//AF009074  
F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence  
./1.2e-131:353:93//AF053356  
F-HEMBB1000598//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.1e-58:600:72//AC006207  
F-HEMBB1000623//cDNA encoding Coliolum manganese peroxidase.//0.89:284:62//E12284  
F-HEMBB1000630//Mus musculus clone NSAT47 nonsatellite RNA sequence.//1.9e-15:129:87//U26231  
F-HEMBB1000631//Sequence 26 from patent US 5708157.//3.2e-27:180:88//I80057  
F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds.//1.6e-48:811:65//AB002349  
F-HEMBB1000637//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.1e-58:649:73//AC005478  
F-HEMBB1000638//HS\_3051\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=M, genomic survey sequence.//0.0032:497:56//AQ155234  
F-HEMBB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:791:68//AC005077  
F-HEMBB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//5.2e-64:775:69//AC003009  
F-HEMBB1000652//Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.7e-52:334:89//AC006186  
F-HEMBB1000665//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//0.0062:426:60//AL024493  
F-HEMBB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contain

ns ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//9.6e-95:399:78//Z84488

F-HEMBB1000673//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//3.8e-50:293:92//AQ155121

F-HEMBB1000684//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SEQUENCE.//8.0e-65:282:83//Z93241

F-HEMBB1000693//Homo sapiens neuroan1 mRNA, complete cds.//1.6e-118:575:97//AF040723

F-HEMBB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.6e-07:251:61//AC005507

F-HEMBB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//2.9e-20:434:64//AL031118

F-HEMBB1000709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//0.26:184:65//AL034554

F-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//1.8e-129:692:93//U53475

F-HEMBB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.7e-40:304:80//U91321

F-HEMBB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//8.9e-35:582:63//AF011889

F-HEMBB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//6.2e-46:262:89//AC005849

F-HEMBB1000763//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//1.6e-99:316:98//AL034405

F-HEMBB1000770//Human DNA sequence from clone 80I19 on chromosome 6p21.3

1-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//0.044:325:60//AL022727  
 F-HEMBB1000774  
 F-HEMBB1000781//Sequence 3 from patent US 5753446.//1.2e-92:599:86//AR008277  
 F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds.//9.3e-64:672:71//AB014577  
 F-HEMBB1000790//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.4e-41:460:74//AC004801  
 F-HEMBB1000794//HS\_3034\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence.//1.8e-74:378:97//AQ117099  
 F-HEMBB1000807//H.sapiens CpG island DNA genomic MseI fragment, clone 39d7, reverse read cpg39d7.rtl1a.//8.5e-14:95:97//Z58412  
 F-HEMBB1000810//H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 303a8, complete read.//3.2e-05:138:71//Z79983  
 F-HEMBB1000821//HS\_2168\_B1\_A12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey sequence.//0.85:208:60//AQ086361  
 F-HEMBB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence.//3.0e-06:361:60//AC003015  
 F-HEMBB1000826//Human BAC clone RG180F08 from 7q31, complete sequence.//1.1e-27:360:69//AC002431  
 F-HEMBB1000827  
 F-HEMBB1000831  
 F-HEMBB1000835//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//0.00098:234:63//AL023581

F-HEMBB1000840//Human Chromosome 11 Cosmid cSRL97a6, complete sequence./  
/4.5e-61:328:79//U73649

F-HEMBB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome  
1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitoc  
hondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unk  
nown gene and the last exon of the JEM1 gene coding for the Basic-Leucin  
e Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end seque  
nce (GSS), complete sequence.//9.7e-144:809:87//AL021068

F-HEMBB1000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic  
sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.12:492:58//AC0  
04157

F-HEMBB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic  
sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0024:212:67//A  
C004157

F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds.//1.5e-32:200:94/  
/AF085351

F-HEMBB1000883//HS\_3065\_B2\_C04\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3065 Col=8 Row=F, genomic survey s  
equence.//0.0017:152:66//AQ137687

F-HEMBB1000887

F-HEMBB1000888//CIT-HSP-2329A10.TR CIT-HSP Homo sapiens genomic clone 23  
29A10, genomic survey sequence.//1.5e-31:172:98//AQ044369

F-HEMBB1000890

F-HEMBB1000893//Plasmodium falciparum MAL3P2, complete sequence.//9.5e-0  
6:768:56//AL034558

F-HEMBB1000908//Homo sapiens clone DJ1119N05, complete sequence.//4.5e-2  
1:199:82//AC004968

F-HEMBB1000910//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL4P1, WORKING DRAFT SEQUENCE.//0.72:366:59//AL034557



F-HEMBB1000913//HS\_3078\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//9.9e-12:221:63//AQ144507

F-HEMBB1000915//Homo sapiens DNA for (CGG)<sub>n</sub> trinucleotide repeat region, isolate P4.//1.2e-49:252:99//AJ001215

F-HEMBB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H62), complete sequence.//2.3e-42:316:76//AC006077

F-HEMBB1000927//Human BDR-2 mRNA for hippocalcin, complete cds.//3.6e-30:528:65//D16593

F-HEMBB1000947//CpG0856B CpIOWAgDNA1 Cryptosporidium parvum genomic, genomic survey sequence.//0.81:262:62//AQ254493

F-HEMBB1000959//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING DRAFT SEQUENCE.//1.2e-43:454:75//Z84487

F-HEMBB1000973//Mus musculus schlafen2 (Slfn2) mRNA, complete cds.//8.3e-42:458:72//AF099973

F-HEMBB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MBK5, complete sequence.//0.98:196:63//AB005234

F-HEMBB1000981

F-HEMBB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//2.9e-06:566:57//AC004476

F-HEMBB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//0.099:391:57//Z98753

F-HEMBB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//6.2e-33:227:80//Z94802

F-HEMBB1001004

F-HEMBB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.//4.0e-13:164:79//AC002551

F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//7.5e-13:229:69//AC002310

F-HEMBB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LANL), complete sequence.//0.32:474:58//AC005751

F-HEMBB1001020//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.6e-39:218:80//AF069291

F-HEMBB1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//5.3e-05:656:59//AF070717

F-HEMBB1001037//CIT-HSP-2358K16.TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey sequence.//6.6e-05:228:64//AQ080539

F-HEMBB1001047//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//4.0e-27:385:71//U82671

F-HEMBB1001051//H.sapiens mRNA for FAN protein.//1.2e-27:160:98//X96586

F-HEMBB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-89:180:91//AC006014

F-HEMBB1001058//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-41:468:74//AC006060

F-HEMBB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.3e-122:785:86//U49973

F-HEMBB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING DRAFT SEQUENCE.//7.1e-162:770:99//AL034375

F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:736:95//AF034803

F-HEMBB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gida) genes, complete cds; and termination factor Rho (rho) gene, partial cds.//0.00088:690:57//AF008210

F-HEMBB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//2.1e-76:368:99//AF049612

F-HEMBB1001105//CIT-HSP-2185N1.TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence.//1.0e-09:136:76//AQ002987

F-HEMBB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630

F-HEMBB1001114//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//7.2e-07:459:59//AC005284

F-HEMBB1001117//HS\_2178\_B1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence.//7.8e-50:331:86//AQ068244

F-HEMBB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.//1.6e-25:150:98//U73778

F-HEMBB1001126

F-HEMBB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.8e-24:228:80//AC004673

F-HEMBB1001137

F-HEMBB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.0e-40:231:76//AC004617

F-HEMBB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264

F-HEMBB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.//0.76:136:67//AQ075724

F-HEMBB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//9.9e-63:259:79//AL008712

F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509:66//D78334

F-HEMBB1001177//CIT-HSP-2321I17.TR CIT-HSP Homo sapiens genomic clone 2321I17, genomic survey sequence.//5.9e-27:320:75//AQ036473

F-HEMBB1001182//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-1

1-30J5, genomic survey sequence.//5.7e-06:62:96//B85188  
F-HEMBB1001199  
F-HEMBB1001208//HS\_2026\_B1\_C07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237  
F-HEMBB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357  
F-HEMBB1001210//HS\_3102\_A2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196  
F-HEMBB1001218//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291  
F-HEMBB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504  
F-HEMBB1001234//H.sapiens CpG island DNA genomic MseI fragment, clone 39f9, forward read cpg39f9.ftle.//4.0e-30:171:97//Z65435  
F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754  
F-HEMBB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087  
F-HEMBB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032  
F-HEMBB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey sequence.//3.7e-54:284:97//AQ037173  
F-HEMBB1001267//Homo sapiens chromosome 17, clone hRPK.488\_L\_1, complete sequence.//3.5e-30:236:78//AC005303  
F-HEMBB1001271//HS\_3011\_A1\_G02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey s

equence.//5.2e-07:364:62//AQ214217

F-HEMBB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 2356J20, genomic survey sequence.//1.8e-16:109:97//AQ060969

F-HEMBB1001288//R.norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366

F-HEMBB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:434:74//AC000387

F-HEMBB1001294//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//2.0e-90:437:99//AQ155035

F-HEMBB1001302

F-HEMBB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15, genomic survey sequence.//2.2e-07:370:61//B69144

F-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//5.7e-116:663:85//U92703

F-HEMBB1001315//Homo sapiens chromosome 10 clone LA10NC01\_40\_G\_3.map 10q26.1-10q26.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:77//AC006096

F-HEMBB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.4e-122:680:91//AC006210

F-HEMBB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.8e-09:518:60//AC004129

F-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//3.7e-56:458:79//D63850

F-HEMBB1001335//HS\_3055\_A1\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=19 Row=0, genomic survey sequence.//1.0:222:63//AQ147384

F-HEMBB1001337//Human PAC clone DJ0093I03 from Xq23, complete sequence.//1.0e-74:319:85//AC003983

F-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region

.//4.0e-135:856:87//U85056  
 F-HEMBB1001346//Human familial Alzheimer's disease (STM2) gene, complete  
 cds.//3.3e-44:481:74//U50871  
 F-HEMBB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-pl5, complete  
 sequence.//1.8e-17:210:73//AC006041  
 F-HEMBB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 u  
 nordered pieces.//1.0:386:59//AC005079  
 F-HEMBB1001364//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complet  
 e sequence.//0.97:349:61//AC004662  
 F-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p  
 11.2-10p12.1, complete sequence.//5.5e-161:766:98//AC005876  
 F-HEMBB1001367//Homo sapiens chromosome 17, clone hRPC.906\_A\_24, complet  
 e sequence.//3.0e-55:510:76//AC004408  
 F-HEMBB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequ  
 ence.//0.048:244:64//AC005192  
 F-HEMBB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, comp  
 lete sequence.//2.5e-26:257:78//AC006204  
 F-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, comple  
 te cds.//5.1e-99:571:89//AF071314  
 F-HEMBB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA ge  
 ne.//7.1e-05:546:58//X02354  
 F-HEMBB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete  
 sequence.//4.0e-129:788:88//AC005023  
 F-HEMBB1001410//Homo sapiens wbscr1 (WBSCR1) and replication factor C su  
 bunit 2 (RFC2) genes, complete cds.//4.8e-11:632:59//AF045555  
 F-HEMBB1001424//Mus musculus Chromosome 4 BAC clone BacB6, complete sequ  
 ence.//0.0012:435:59//AC003019  
 F-HEMBB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5  
 unordered pieces.//3.8e-17:360:64//AC005482

F-HEMBB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt]./  
/4.1e-114:668:88//S65367

F-HEMBB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.  
3e-37:438:74//AB000931

F-HEMBB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, comp  
lete cds.//9.1e-92:550:88//L18966

F-HEMBB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142),  
complete sequence.//0.00024:385:62//AC004768

F-HEMBB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequ  
ence.//0.84:577:57//AC005790

F-HEMBB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENC  
E, 11 unordered pieces.//8.0e-40:377:78//AC000382

F-HEMBB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete  
sequence.//0.011:482:59//AF001549

F-HEMBB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete s  
equence.//0.019:263:61//U91320

F-HEMBB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein  
Roaz mRNA, alternatively spliced form, complete cds.//1.0e-30:521:66//U  
92564

F-HEMBB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//1.3e-31:479:71//AC004873

F-HEMBB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 u  
nordered pieces.//3.7e-51:680:70//AC005080

F-HEMBB1001527

F-HEMBB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCR  
Region, complete sequence.//1.3e-79:696:79//AC000089

F-HEMBB1001535//O.aries DNA for polymorphic marker 'OVINRA01' (339 bp)./  
/0.00034:217:62//X89268

F-HEMBB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, com

plete sequence.//0.54:266:60//AC004548

F-HEMBB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784:61//AC004262

F-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//6.9e-50:213:80//AC004605

F-HEMBB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269:60//AC005041

F-HEMBB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//1.7e-107:620:83//AL020989

F-HEMBB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734:67//AC004003

F-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.4e-166:816:97//AL031677

F-HEMBB1001586

F-HEMBB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419:65//AC005261

F-HEMBB1001603

F-HEMBB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//4.5e-29:422:72//Z99289

F-HEMBB1001619//HS\_3079\_B1\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77:79//AQ123388

F-HEMBB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 u



ordered pieces.//3.2e-12:667:59//AC005089

F-HEM BB1001635//Plasmodium falciparum MAL3P7, complete sequence.//3.8e-05:475:57//AL034559

F-HEM BB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//9.2e-13:168:76//AL021155

F-HEM BB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MP012, complete sequence.//0.00097:721:58//AB006702

F-HEM BB1001653//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//0.15:276:63//AC002038

F-HEM BB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.43:393:61//L14320

F-HEM BB1001668//F16C15-T7 IGF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//0.040:275:60//B12308

F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803:98//AB014546

F-HEM BB1001684//Sequence 1 from patent US 5700927.//7.5e-124:883:81//I86429

F-HEM BB1001685//CIT-HSP-228709.TF CIT-HSP Homo sapiens genomic clone 228709, genomic survey sequence.//2.3e-34:191:97//B99261

F-HEM BB1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase

yltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LC B-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178

F-HEMBB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575

F-HEMBB1001706

F-HEMBB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543

F-HEMBB1001717//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//1.1e-13:723:58//AJ223323

F-HEMBB1001735//Human PAC clone DJ0596009 from 7p15, complete sequence.//1.3e-36:427:73//AC003074

F-HEMBB1001736//S.pombe chromosome II cosmid c4B4.//0.0085:479:57//AL023706

F-HEMBB1001747//Homo sapiens PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376

F-HEMBB1001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.3e-98:395:82//AC005829

F-HEMBB1001753//S.maximus repeat region, 342bp.//4.2e-11:69:85//Z78099

F-HEMBB1001756//Homo sapiens full length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064

F-HEMBB1001760//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275

F-HEMBB1001762//CIT-HSP-2290J16.TF CIT-HSP Homo sapiens genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184

F-HEMBB1001785//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746

F-HEMBB1001797//Human heterogenous nuclear RNA W16W.//0.00012:83:86//X17272

F-HEMBB1001802//Plasmodium falciparum MAL3P7, complete sequence.//1.8e-11:538:60//AL034559

F-HEMBB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882

F-HEMBB1001816//Homo sapiens chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204

F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCI P1) mRNA, complete cds.//2.3e-162:763:98//AF056209

F-HEMBB1001834//CIT-HSP-2291012.TF CIT-HSP Homo sapiens genomic clone 2291012, genomic survey sequence.//7.6e-08:73:94//AQ004168

F-HEMBB1001836//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801

F-HEMBB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073

F-HEMBB1001850//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//AC005504

F-HEMBB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581

F-HEMBB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563

F-HEMBB1001868//Rattus norvegicus clone 923 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145

F-HEMBB1001869//Homo sapiens full length insert cDNA clone YT86F01.//7.4e-87:432:97//AF085974

F-HEMBB1001872

F-HEMBB1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 u

nordered pieces.//3.4e-14:631:61//AC005000

F-HEMBB1001875//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209

F-HEMBB1001880//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403

F-HEMBB1001899//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//0.0038:425:58//AL010216

F-HEMBB1001905//S.pombe chromosome III cosmid c330.//1.1e-23:520:62//AL031603

F-HEMBB1001906

F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//3.7e-82:672:81//U47742

F-HEMBB1001910//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505

F-HEMBB1001911//Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence.//1.0:581:58//AC004705

F-HEMBB1001915//Caenorhabditis elegans cosmid T05H10, complete sequence.//1.2e-16:283:67//Z47812

F-HEMBB1001921//Homo sapiens chromosome 17, clone hCIT.123\_J\_14, complete sequence.//3.4e-07:803:58//AC003950

F-HEMBB1001922//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//5.0e-06:756:56//AE001391

F-HEMBB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.1e-45:609:73//AL009181

F-HEMBB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11

./3.2e-158:745:99//AB020867

F-HEM BB1001944//, complete sequence./4.1e-60:638:73//AC005815

F-HEM BB1001945//HS\_3185\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence./1.0:280:58//AQ188882

F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds./5.6e-20:333:66//AB002390

F-HEM BB1001950//Human lipocortin (LIP) 2 gene, upstream region./0.0094:180:63//M62899

F-HEM BB1001952//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 101A4, WORKING DRAFT SEQUENCE./5.4e-19:329:70//Z93341

F-HEM BB1001953//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence./0.11:589:58//AC005284

F-HEM BB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island./9.8e-25:446:67//Z98941

F-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence./2.8e-147:727:97//AC005736

F-HEM BB1001967//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces./3.2e-56:650:71//AC004963

F-HEM BB1001973//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces./1.2e-42:327:84//AC005844

F-HEM BB1001983//CIT-HSP-2315M4.TF CIT-HSP Homo sapiens genomic clone 2315M4, genomic survey sequence./8.8e-35:198:96//AQ028071

F-HEM BB1001988//D.polychroa microsatellite sequence (clone Dp 1C e12)./4.5e-07:337:62//X92189

F-HEM BB1001990//HS\_3234\_A1\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=15 Row=M, genomic survey

sequence.//0.039:279:59//AQ204689

F-HEMBB1001996//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507

F-HEMBB1001997//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069

F-HEMBB1002002//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153

F-HEMBB1002005//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685

F-HEMBB1002009//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00033:790:56//AC005506

F-HEMBB1002015//Homo sapiens genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05:126:76//AP000056

F-HEMBB1002042//Oncorhynchus mykiss cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69//AF046012

F-HEMBB1002043

F-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//3.0e-167:809:97//AC005740

F-HEMBB1002045

F-HEMBB1002049//Homo sapiens chromosome 17, clone hRPC.161\_P\_9, complete sequence.//0.87:177:65//AC006237

F-HEMBB1002050//Streptomyces coelicolor cosmid D78.//8.5e-08:644:58//AL034355

F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:61//AB014512

F-HEMBB1002069

F-HEMBB1002092//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4

, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064

F-HEMBB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence.//2.9e-49:302:83//AG001476

F-HEMBB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//0.00023:542:61//AC004035

F-HEMBB1002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3e-43:533:70//U43843

F-HEMBB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714

F-HEMBB1002142//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748

F-HEMBB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421

F-HEMBB1002189//Homo sapiens cosmid ICRFc104I0935Q8 from Xq28, complete sequence.//2.6e-05:311:63//AF002998

F-HEMBB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140

F-HEMBB1002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I80846

F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10.//1.2e-23:405:67//X52332

F-HEMBB1002218//HS\_2056\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711

F-HEMBB1002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9e-21:314:70//U73648

F-HEMBB1002247.

F-HEMBB1002249//Homo sapiens DNA sequence from BAC 3418 on chromosome 6p 21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs, STSS and GSSs, complete sequence.//4.1e-45:327:83//AL021918

F-HEMBB1002254//Human chromosome 16 BAC clone LANL cosmid-440E5, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.8e-40:315:82//AC002506

F-HEMBB1002255//Plasmodium falciparum MAL3P3, complete sequence.//0.0035:312:62//Z98547

F-HEMBB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:469:59//AC005504

F-HEMBB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//5.3e-18:527:61//AC004682

F-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//8.6e-139:818:88//U73642

F-HEMBB1002306//HS\_3109\_A2\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=0, genomic survey sequence.//1.3e-75:371:98//AQ148164

F-HEMBB1002327//HS\_3235\_B2\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=N, genomic survey sequence.//3.3e-83:418:97//AQ209752

F-HEMBB1002329//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//3.3e-31:220:88//AQ263402

F-HEMBB1002340

F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.



//4.1e-154:724:98//AJ010841

F-HEMBB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds.//3.3e-36:192:98//L16991

F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds.//1.8e-13:96:96//U55766

F-HEMBB1002364//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 376D21, WORKING DRAFT SEQUENCE.//7.5e-24:202:71//Z98946

F-HEMBB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-06:674:56//AC004153

F-HEMBB1002381//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222

F-HEMBB1002383

F-HEMBB1002387//CIT-HSP-2173E20.TR CIT-HSP Homo sapiens genomic clone 21 73E20, genomic survey sequence.//5.2e-17:434:66//B91052

F-HEMBB1002409//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712

F-HEMBB1002415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//8.9e-35:334:75//AL031319

F-HEMBB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//1.0e-36:317:76//U62317

F-HEMBB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//U92010

F-HEMBB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING DRAFT SEQUENCE.//2.7e-43:419:78//AL034349

F-HEMBB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.3e-27:542:68//AC005534

F-HEMBB1002458//HS\_3246\_A2\_G05\_MR CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3246 Col=10 Row=M, genomic survey  
sequence.//3.2e-51:257:99//AQ217993  
F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e  
-87:493:92//U43885  
F-HEMBB1002489  
F-HEMBB1002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919  
F-HEMBB1002495//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complet  
e sequence.//1.1e-16:297:68//AC006141  
F-HEMBB1002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-9  
1:675:82//AC005230  
F-HEMBB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, c  
omplete sequence.//2.7e-11:648:60//AC004605  
F-HEMBB1002510//HS\_3236\_B1\_H11\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3236 Col=21 Row=P, genomic survey  
sequence.//1.2e-06:67:94//AQ205992  
F-HEMBB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequen  
ce.//1.2e-70:580:72//AC006152  
F-HEMBB1002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Syst  
ems Human BAC library) complete sequence.//5.6e-22:516:64//AC004553  
F-HEMBB1002531  
F-HEMBB1002534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 668J24, WORKING DRAFT SEQUENCE.//6.9e-62:265:87//AL034346  
F-HEMBB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequen  
ce.//2.7e-44:200:82//AC000059  
F-HEMBB1002550//Homo sapiens PAC clone DJ0910I17 from 7q11.21-q11.23, co  
mplete sequence.//0.22:161:68//AC004927  
F-HEMBB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete  
sequence.//7.5e-43:306:77//AC004861  
F-HEMBB1002579

F-HEM BB1002582//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 349A12, WORKING DRAFT SEQUENCE.//0.00018:431:61//AL033520

F-HEM BB1002590//Yeast (*S.cerevisiae*) mitochondrial apocytochrome b gene,  
3' flank.//0.78:147:64//J01471

F-HEM BB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 9E21, WORKING DRAFT SEQUENCE.//3.6e-50:692:69//AL008639

F-HEM BB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-1  
51:710:98//AF089749

F-HEM BB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//  
1.5e-07:416:60//AC002381

F-HEM BB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequenc  
e.//0.40:341:60//AC002454

F-HEM BB1002607//Mus musculus homeobox containing nuclear transcriptional  
factor Hmx1 (*Hmx1*) gene, complete cds.//0.0042:460:60//AF009614

F-HEM BB1002610//Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell P  
ark Cancer Institute Human PAC library) complete sequence.//6.3e-23:559:  
63//AC003029

F-HEM BB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete  
sequence.//4.2e-17:441:63//AC000025

F-HEM BB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of  
the complete sequence.//0.013:324:56//AE001417

F-HEM BB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 com  
plete sequence.//2.1e-07:441:60//AF001550

F-HEM BB1002623//C.hyalina microsatellite marker DNA (id ATCC4).//0.57:10  
6:66//Z95304

F-HEM BB1002635//Human JNK3 alpha2 protein kinase (*JNK3A2*) mRNA, complete  
cds.//4.8e-22:127:100//U34819

F-HEM BB1002664//HS\_2265\_A1\_H06\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2265 Col=11 Row=0, genomic survey

sequence.//0.54:115:67//AQ101557

F-HEMBB1002677//Homo sapiens (subclone 3\_d1 from P1 H25) DNA sequence, complete sequence.//2.2e-49:784:68//L81774

F-HEMBB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23.//1.0:112:63//U04492

F-HEMBB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 772 Col=12 Row=M, genomic survey sequence.//4.4e-07:86:84//B39748

F-HEMBB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=20 Row=L, genomic survey sequence.//0.98:183:61//B34077

F-HEMBB1002692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING DRAFT SEQUENCE.//0.00039:408:60//AL033525

F-HEMBB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.3e-35:323:74//AC004955

F-HEMBB1002699//Mus musculus D6MM5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and LOR2 protein (Lor2) gene, partial cds.//0.031:325:62//AF084363

F-HEMBB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=2 Row=G, genomic survey sequence.//1.8e-25:158:95//B34720

F-HEMBB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//1.7e-137:534:96//AB003151

F-HEMBB1002712//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//0.0019:612:58//Z71187

F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.1e-43:354:81//AC003117

F-MAMMA1000019

F-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//2.0e-40:185:97//Z47553

F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-pl4, complete sequence.//1.0:211:65//AC005483

F-MAMMA1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12.//0.075:204:65//M73275

F-MAMMA1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.1e-122:495:79//AL031073

F-MAMMA1000055//M.musculus mRNA for testin.//2.1e-35:559:66//X78989

F-MAMMA1000057//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//5.5e-121:703:89//AC005829

F-MAMMA1000069//Homo sapiens minisatellite ceb1 repeat region.//0.00013:329:60//AF048727

F-MAMMA1000084//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.1e-53:445:79//Z93023

F-MAMMA1000085//Caenorhabditis elegans cosmid Y23H5A.//0.0017:164:64//AF077541

F-MAMMA1000092//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//1.2e-70:598:78//AC004744

F-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.1e-156:857:92//AC003976

F-MAMMA1000117//HS\_3223\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=16 Row=H, genomic survey sequence.//5.4e-100:527:94//AQ221160

F-MAMMA1000129//ryanodine receptor.//0.055:492:59//A20359

F-MAMMA1000133

F-MAMMA1000134//HS\_3078\_B1\_C02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//2.1e-93:462:97//AQ144362

F-MAMMA1000139//Homo sapiens Xp22 PAC RPC11-5G11 (from Roswell Park Cancer Center) complete sequence.//3.3e-14:322:65//AC002369

F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds.//6.9e-25:148:97//AB014585

F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds.//1.0e-29:219:87//AF031924

F-MAMMA1000163

F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//6.3e-14:92:88//AC005393

F-MAMMA1000173//Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin.//2.2e-114:698:87//U58884

F-MAMMA1000175//HS\_3050\_B1\_B03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=5 Row=D, genomic survey sequence.//6.2e-73:357:99//AQ102678

F-MAMMA1000183//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//4.6e-94:904:73//AL023808

F-MAMMA1000198//Z.diploperennis repetitive DNA (clone ZEAR 266).//0.18:152:70//X53610

F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.017:99:75//AC004583

F-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//0.36:312:62//AL031283

F-MAMMA1000241//HS\_3217\_B1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=3 Row=D, genomic survey sequence.//1.9e-94:456:98//AQ193401

F-MAMMA1000251//Homo sapiens NF2 gene.//0.00092:270:64//Y18000  
F-MAMMA1000254//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0034:777:57//AC005140  
F-MAMMA1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome 6 p22.1-22.3. Contains EST and STS.//0.00036:230:65//AL022717  
F-MAMMA1000264//Homo sapiens (subclone 9\_f5 from P1 H17) DNA sequence, complete sequence.//1.5e-30:499:68//L81612  
F-MAMMA1000266//Bacillus lynceorum strain pMEL12 Bag320 satellite DNA.//0.28:218:64//AF034430  
F-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.4e-157:788:96//AF001549  
F-MAMMA1000277//Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.//0.70:320:61//AL021897  
F-MAMMA1000278//Sequence 23 from patent US 5708157.//9.3e-103:540:95//I80055  
F-MAMMA1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, STS, GSS, complete sequence.//2.4e-49:262:77//AL031643  
F-MAMMA1000284//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//1.1e-30:324:75//B03004  
F-MAMMA1000287//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//2.7e-54:401:83//AC006213  
F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome.//0.0051:307:61//U37541  
F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPCI5-1154L15, WORKING DRAFT SEQUENCE, 67 unordered pieces.//0.15:449:59//AC006205  
F-MAMMA1000309//cDNA coding human apolipoprotein E3.//0.00010:691:58//E0

0359

F-MAMMA1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 798A17, WORKING DRAFT SEQUENCE.//0.27:301:60//AL031274

F-MAMMA1000313

F-MAMMA1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence.//9.8e-06:151:71//AC002400

F-MAMMA1000339

F-MAMMA1000340//HS\_2181\_B2\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181 Col=14 Row=L, genomic survey sequence.//4.3e-05:181:68//AQ024288

F-MAMMA1000348//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//5.3e-30:575:66//AC004139

F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-52:264:76//AC005052

F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//6.5e-91:569:88//AC004879

F-MAMMA1000361//Human DNA sequence from PAC 507115 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//1.4e-42:315:83//Z98950

F-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//2.9e-114:516:89//AL022345

F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//6.9e-26:377:71//AQ279944

F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//3.7e-148:710:98//AB015132

F-MAMMA1000395

F-MAMMA1000402//Homo sapiens clone DJ0718N17, complete sequence.//4.0e-15:845:85//AC005999

F-MAMMA1000410//HS\_3245\_A1\_C02\_MR CIT Approved Human Genomic Sperm Library



ry D Homo sapiens genomic clone Plate=3245 Col=3 Row=E, genomic survey s  
equence.//9.6e-42:350:80//AQ205768

F-MAMMA1000413//HS\_3223\_B2\_F01\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic survey s  
equence.//1.6e-48:318:89//AQ188456

F-MAMMA1000414//HS\_2027\_B2\_C04\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey s  
equence.//1.4e-46:286:92//AQ231369

F-MAMMA1000416//Drosophila melanogaster DNA sequence (Pls DS07528 (D169)  
and DS06665 (D220)), complete sequence.//9.4e-33:310:72//AC004640

F-MAMMA1000421//Homo sapiens clone DJ1129D05, complete sequence.//3.3e-2  
9:223:84//AC005630

F-MAMMA1000422

F-MAMMA1000423//Drosophila yakuba mitochondrial DNA molecule.//2.2e-10:6  
39:57//X03240

F-MAMMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete  
sequence.//4.6e-47:556:68//AC003973

F-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//8.0e-99:545:92//A  
F062484

F-MAMMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3  
unordered pieces.//4.8e-41:289:79//AC005283

F-MAMMA1000444//Human DNA sequence from clone 714B7 on chromosome 22q12.  
2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and  
ESTs, complete sequence.//2.3e-34:291:80//Z99755

F-MAMMA1000446

F-MAMMA1000458//Mus musculus clone OST9003, genomic survey sequence.//5.  
0e-53:231:84//AF046620

F-MAMMA1000468//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 291J10, WORKING DRAFT SEQUENCE.//0.75:303:60//Z93017

F-MAMMA1000472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//4.0e-41:403:77//AL033543

F-MAMMA1000478//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.5e-54:369:77//AC005081

F-MAMMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//3.6e-34:332:77//AC004381

F-MAMMA1000490//Homo sapiens 12q13.1 PAC RPCI1-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//8.9e-128:822:87//AC003686

F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 231905, genomic survey sequence.//4.8e-29:175:94//AQ044812

F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//5.7e-45:334:82//AL022336

F-MAMMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.9e-43:529:69//Z92545

F-MAMMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//2.0e-14:380:63//AL022576

F-MAMMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//1.4e-22:420:66//AC006101

F-MAMMA1000559//Human HepG2 3' region cDNA, clone hmd3f08.//5.4e-29:168:97//D16922

F-MAMMA1000565//RPCI11-61K6.TJ RPCI11 Homo sapiens genomic clone R-61K6, genomic survey sequence.//1.7e-120:561:100//AQ194238

F-MAMMA1000567//Human DNA sequence from PAC 179D3, between markers DXS67 91 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//3.1e-43:387:80//Z81370

F-MAMMA1000576//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.2e-30:237:75//AC005104

F-MAMMA1000583//RPCI11-60M22.TJ RPCI11 Homo sapiens genomic clone R-60M2 2, genomic survey sequence.//9.6e-102:487:99//AQ198091

F-MAMMA1000585//Homo sapiens clone UWGC:djs14 from 7p14-15, complete sequence.//5.2e-39:370:78//AC006195

F-MAMMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete sequence.//3.9e-43:328:83//AC005338

F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete sequence.//1.5e-32:259:82//AC005839

F-MAMMA1000605//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.4e-59:318:83//AL031297

F-MAMMA1000612//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//4.8e-30:171:96//AQ116793

F-MAMMA1000616//HS\_3176\_A1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3176 Col=11 Row=I, genomic survey sequence.//4.7e-28:287:79//AQ300310

F-MAMMA1000621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING DRAFT SEQUENCE.//0.015:478:58//AL034371

F-MAMMA1000623

F-MAMMA1000625//DNA encoding Hepatitis C virus antigen.//0.93:196:61//E06898

F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds.//0.95:365:59//AF023674

F-MAMMA1000664//HS\_3096\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence.//2.7e-51:257:99//AQ145137

F-MAMMA1000669//Homo sapiens chromosome 19, cosmid R26908, complete sequence.//2.0e-66:586:67//AC004785

F-MAMMA1000670//HS\_2243\_B2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence.//8.7e-05:94:80//AQ153650

F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence.//3.9e-64:471:81//AF046705

F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds.//1.2e-07:186:67//U27489

F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration site 2B (EVI2B) exons 1-2; ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-2.//3.0e-53:653:70//L05367

F-MAMMA1000707//CIT-HSP-2302019.TR CIT-HSP Homo sapiens genomic clone 2302019, genomic survey sequence.//1.8e-08:131:77//AQ017947

F-MAMMA1000713//Rattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.062:134:67//U00762

F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end.//1.0:266:61//X15028

F-MAMMA1000718//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//3.6e-05:289:60//B95401

F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//4.4e-184:842:98//AC005781

F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence.//8.8e-05:430:60//AC004917

F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133))

, complete sequence.//3.8e-55:796:66//AC004274

F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.6e-77:55:74//AF064859

F-MAMMA1000733//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//0.98:479:58//AL031749

F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//7.3e-168:802:98//AF100141

F-MAMMA1000738//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-31:626:63//Z71408

F-MAMMA1000744//Gorilla Alu-repetitive sequence in beta-globin gene cluster.//2.7e-54:410:82//X06123

F-MAMMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence.//3.7e-109:779:83//AC004158

F-MAMMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-20:444:63//AC005075

F-MAMMA1000760//Homo sapiens clone RG015P03, complete sequence.//1.5e-44:403:79//AC005048

F-MAMMA1000761//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.3e-22:159:81//AC004166

F-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.3e-51:789:68//AC005703

F-MAMMA1000776//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 contains ESTs, CA repeat, GSS.//5.7e-40:238:78//Z95116

F-MAMMA1000778//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//7.6e-29:222:84//AL031118

F-MAMMA1000782//Human 2,4-dienoyl-CoA reductase gene, exon 9.//0.90:137:62//U94987

F-MAMMA1000798//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chr

osome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.00058:163:71//AC003656

F-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//6.3e-151:714:99//AC005339

F-MAMMA1000824//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC005912

F-MAMMA1000831//Homo sapiens clone UWGC:g1211a139, complete sequence.//0.76:302:58//AC005502

F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//1.9e-54:322:68//AC002456

F-MAMMA1000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755

F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817

F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC004710

F-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557

F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//0.86:193:63//U00146

F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repeat probe, clone lambda 33.10.//0.081:229:62//M30549

F-MAMMA1000856//B.taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z22747

F-MAMMA1000859//Sequence 6 from Patent W09722695.//2.3e-79:533:82//A6355

F-MAMMA1000862

F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21  
/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050

F-MAMMA1000865

F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2  
385J8, genomic survey sequence.//0.00017:158:70//AQ240906

F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome  
Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA re  
peat, STS, complete sequence.//1.0:121:68//AL022152

F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185  
:90//AF015152

F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome  
22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP)  
LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75/  
/AL022336

F-MAMMA1000880//Homo sapiens full length insert cDNA clone ZD54A10.//5.2  
e-26:143:100//AF086327

F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.  
31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801

F-MAMMA1000897//R.norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y  
11283

F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, g  
enomic survey sequence.//0.94:115:66//B61433

F-MAMMA1000906//HS\_3110\_B2\_A11\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey  
sequence.//2.5e-63:548:78//AQ182819

F-MAMMA1000908//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397

F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-0

9:596:58//AL034560

F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//B89575

F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-43:415:66//AC004917

F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296

F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299

F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.8e-14:175:76//AL031117

F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//AC005308

F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.//3.3e-30:530:67//AC004643

F-MAMMA1000957//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//1.3e-72:390:94//AQ155121

F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-58:318:86//AC006001

F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs



, STSS and GSSs, complete sequence.//1.4e-18:396:65//AL022394

F-MAMMA1000975//Human DNA sequence from clone 344I7 on chromosome Xp11.2  
1-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8,  
KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//A  
L024458

F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, comp  
lete sequence.//0.089:214:66//AC004991

F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//  
1.1e-58:458:82//AC000114

F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12.  
Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406

F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq  
21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort prot  
ein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Chor  
oideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains E  
STs and an STS, complete sequence.//0.24:166:68//AL022401

F-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRA  
FT SEQUENCE.//1.6e-103:139:99//AJ011929

F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial  
cds.//6.5e-48:465:76//AF070567

F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clon  
e 2501L21, genomic survey sequence.//1.0:175:62//AQ241701

F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA  
, complete cds.//1.1e-30:753:61//AF061444

F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complet  
e sequence.//7.9e-24:256:76//AC002990

F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 22  
84N21, genomic survey sequence.//0.96:78:75//AQ000903

F-MAMMA1001041//Chicken mRNA for alpha-actinin, complete cds.//2.8e-09:3

55:63//D26597

F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457

F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125

F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169

F-MAMMA1001073//HS\_3046\_A2\_G08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420

F-MAMMA1001074//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733

F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749

F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//2.0e-22:334:69//AC006120

F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155

F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087

F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05:594:60//AC005256

F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019

F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045

F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637

F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence

nce.//3.3e-21:237:73//AF047825

F-MAMMA1001133//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 C  
ontains ESTs, CA repeat, GSS.//0.97:202:63//Z95116

F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986  
nt].//1.6e-84:406:82//S70011

F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosom  
e 22 Contains EST, exon trap, complete sequence.//1.3e-14:182:76//AL0223  
39

F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers  
DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//5.2e-87:714  
:78//Z71187

F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 23  
41D13, genomic survey sequence.//0.00051:249:61//AQ055735

F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing  
the RAD51L1 gene, complete sequence.//2.2e-30:410:70//AC004518

F-MAMMA1001162//Homo sapiens full length insert cDNA clone ZA79C01.//2.4  
e-13:87:100//AF086123

F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds.//9.3e-15:4  
32:60//U31629

F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complet  
e sequence.//6.8e-57:670:72//AC005696

F-MAMMA1001191

F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//1.5e-117:759:84  
//U29156

F-MAMMA1001202

F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING  
DRAFT SEQUENCE, 2 ordered pieces.//1.5e-161:764:98//AC005412

F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete s  
equence.//5.1e-30:535:65//AC004099

F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//8.4e-182:860:98//AC005393

F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.7e-58:690:70//AC004875

F-MAMMA1001222//Mouse loricrin mRNA, complete cds.//2.7e-07:624:58//M34398

F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.91:177:66//AC005726

F-MAMMA1001244

F-MAMMA1001249//Human 28S ribosomal RNA psuedogenes and alu repeat region sequence.//6.7e-09:502:58//U67616

F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 C contains STS, GSS, complete sequence.//5.0e-37:342:80//Z99495

F-MAMMA1001259

F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//8.7e-40:659:64//AB014561

F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//4.9e-43:265:81//AC004453

F-MAMMA1001271//Salmo salar DNA for a cryptic repeat.//2.6e-06:311:63//AJ012206

F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.6e-70:327:83//AC004840

F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-05:276:66//AC003035

F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a p

utative CpG island, ESTs, and GSSs, complete sequence.//3.6e-98:199:98//  
AL022314

F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapiens genomic clone RPCI-1  
1-38B4, genomic survey sequence.//4.7e-33:292:71//AQ030084

F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complet  
e sequence.//1.6e-182:860:98//AC005703

F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13.  
Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Act  
ivating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D2  
2S1168 and a CA repeat polymorphism, complete sequence.//1.9e-70:163:97/  
/Z93244

F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24.  
1-24.3 Contains protein similar to pregnancy-associated plasma protein A  
precursor neuronal migration protein astrotactin, ESTs, STS and GSS, co  
mplete sequence.//2.6e-19:379:68//AL031290

F-MAMMA1001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 197L1, WORKING DRAFT SEQUENCE.//4.5e-131:751:90//AL031390

F-MAMMA1001330

F-MAMMA1001341//Sus scrofa.//1.6e-36:420:73//Z46906

F-MAMMA1001343//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL1P1, WORKING DRAFT SEQUENCE.//1.1e-05:818:58//AL031744

F-MAMMA1001346

F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered piece  
s.//2.0e-44:505:74//AC004086

F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit a  
mRNA, complete cds.//1.5e-07:415:58//M86826

F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11.  
21-12.1 Contains EST, STS and GSS, complete sequence.//1.6e-23:209:75//A  
L022332

F-MAMMA1001408//HS\_3242\_A1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=21 Row=0, genomic survey sequence.//2.7e-07:181:69//AQ207300

F-MAMMA1001411//Homo sapiens autosomal dominant polycystic kidney disease type II protein (PKD2) gene, exon 14.//0.98:120:68//AF004872

F-MAMMA1001419//HS\_2053\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence.//1.9e-75:424:93//AQ244585

F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete sequence.//2.4e-09:199:70//AC004049

F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-20110 4, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-42:558:69//AC004529

F-MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence.//0.0019:516:56//AE001400

F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.6e-42:486:70//AC003684

F-MAMMA1001452//RPCI11-48022.TJ RPCI11 Homo sapiens genomic clone R-4802 2, genomic survey sequence.//5.3e-87:423:98//AQ199294

F-MAMMA1001465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543

F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:87//L31783

F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0e-13:158:77//AC005486

F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366

F-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714

F-MAMMA1001510//Human PAC clone DJ43804 from 22q12.1-qter, complete sequ

ence.//1.1e-05:371:61//AC002378

F-MAMMA1001522

F-MAMMA1001547

F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:98//AB007931

F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//0.97:154:68//AF001548

F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91//M61764

F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, c complete sequence.//1.8e-07:104:84//Z98949

F-MAMMA1001600//HS\_3022\_A2\_H01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=0, genomic survey s equence.//1.6e-66:405:90//AQ163791

F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA repeat, Ninenin like sequence, complete sequence.//0.00043:715:58//AL008626

F-MAMMA1001606//jd114 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 2G6, genomic survey sequence.//0.19:266:62//B13685

F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds.//9.7e-54:442:69//AF053630

F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive site.//0.14:221:62//M29833

F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.0e-47:611:71//AC005412

F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:67//U57796

F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete sequen

ce.//4.0e-35:407:70//AC000118

F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSS and GSSs, complete sequence.//0.44:245:63//AL022577

F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284

F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence.//9.7e-05:146:66//B95491

F-MAMMA1001670//HS\_3136\_A1\_G06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779

F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614

F-MAMMA1001679//HS\_3054\_A1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=0, genomic survey sequence.//1.0:89:70//AQ106118

F-MAMMA1001683//Spermatozopsis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970

F-MAMMA1001686//HS\_3219\_B1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345

F-MAMMA1001692//HS\_3047\_B1\_B10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228

F-MAMMA1001711//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-42:316:82//AC004845

F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 23



47A14, genomic survey sequence.//1.1e-60:413:87//AQ059125

F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133:646:97//AF095687

F-MAMMA1001735//chicken brain tubulin beta chain mrna.//3.5e-110:740:84//J00913

F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS.//0.98:416:57//Z72001

F-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence.//3.2e-16:194:75//AC006017

F-MAMMA1001744//Homo sapiens DNA sequence from clone 466I8 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998

F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718

F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds.//1.2e-35:583:65//U90065

F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//8.4e-102:627:87//AF041338

F-MAMMA1001757//HS\_2058\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865

F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//6

.6e-76:349:87//AL022722

F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.23:633:57//M97514

F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801

F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801

F-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.7e-106:744:82//X85991

F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence.//6.0e-20:228:75//AC002563

F-MAMMA1001785

F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSS and GSSs, complete sequence.//5.0e-05:152:74//Z99129

F-MAMMA1001790//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//4.5e-53:318:80//AC005845

F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262

F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence.//3.0e-34:257:83//AC004383

F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128

F-MAMMA1001817//Homo sapiens 12q24 PAC RPCI1-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031

1

F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L1  
5, BAC clone 7B7, complete sequence bases 1..333303.//0.71:179:67//AJ011  
930

F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//3.0e-91:726:79/  
/Y13148

F-MAMMA1001824//HS\_3108\_A1\_G12\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3108 Col=23 Row=M, genomic survey  
sequence.//3.4e-05:119:74//AQ107508

F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537\_E\_1, complete  
sequence.//3.4e-45:312:85//AC006211

F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA,  
complete cds.//4.5e-51:480:75//AF052042

F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 Homo sapiens genomic clone  
2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620

F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmid  
s R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:6  
7//AC002390

F-MAMMA1001854

F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 Homo sapiens genomic clone RPCI-  
11-11L22, genomic survey sequence.//0.091:161:65//B75631

F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence./  
/2.6e-09:397:61//AC003013

F-MAMMA1001868//HS\_2196\_B2\_A12\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2196 Col=24 Row=B, genomic survey  
sequence.//5.8e-13:86:100//AQ032455

F-MAMMA1001874//H.sapiens CpG island DNA genomic MseI fragment, clone 63  
h5, reverse read cpg63h5.rt1a.//1.0:127:63//Z62129

F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3  
. Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802

F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 Homo sapiens genomic clone R-90K3,  
genomic survey sequence.//6.6e-11:362:62//AQ283465

F-MAMMA1001890//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 508I15, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL021707

F-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207

F-MAMMA1001908//HS\_2225\_A1\_A03\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2225 Col=5 Row=A, genomic survey s  
equence.//5.4e-08:264:62//AQ301597

F-MAMMA1001931//HS\_3049\_B2\_D09\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey  
sequence.//1.7e-47:295:90//AQ100157

F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493

F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds./  
/0.99:173:68//AF106656

F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers D  
XS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene  
.//5.3e-63:479:78//Z73986

F-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, compl  
ete sequence.//1.4e-126:699:93//AC003071

F-MAMMA1001992//HS\_3078\_A1\_A09\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey  
sequence.//3.3e-08:257:65//AQ143646

F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214\_0\_1, complete  
sequence.//1.5e-07:244:62//AC005224

F-MAMMA1002011//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey s  
equence.//1.3e-07:170:69//AQ304711

F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE,

37 unordered pieces.//2.1e-34:315:79//AC004803

F-MAMMA1002033//HS\_3023\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105493

F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence.//5.3e-85:439:82//AC001227

F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//1.4e-20:314:70//AC005669

F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPCI11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC005906

F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996

F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC004869

F-MAMMA1002068//Homo sapiens, clone hRPK.2\_A\_1, complete sequence.//5.4e-41:407:78//AC006197

F-MAMMA1002078//Human DNA sequence from PAC 106I20 on chromosome 22q12 C contains ESTs and STS, complete sequence.//0.021:333:64//Z81313

F-MAMMA1002082

F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence.//0.032:469:58//Z93380

F-MAMMA1002093//HS\_3050\_B1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey

sequence.//1.0:77:71//AQ105997

F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5' UTR.//8.3e-10:464:60//AF017308

F-MAMMA1002118

F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.//1.0e-35:619:68//AC003962

F-MAMMA1002132//RPCI11-78F11.TJ RPCI11 Homo sapiens genomic clone R-78F11, genomic survey sequence.//1.0e-90:357:97//AQ286460

F-MAMMA1002140//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216

F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338

F-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391

F-MAMMA1002153//HS\_3005\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213

F-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462023, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431

F-MAMMA1002156

F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence.//7.1e-42:255:92//AQ266165

F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//2.0e-81:604:81//AC004448

F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212

F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548

F-MAMMA1002209//HS\_2197\_B1\_E07\_MR CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey  
sequence.//9.6e-18:163:84//AQ210058

F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and c  
omplete 5' UTR.//6.3e-08:435:60//AF017308

F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.8e-124:7  
52:87//AF032667

F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic  
sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC0  
04710

F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit  
(eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253

F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complet  
e sequence.//1.4e-145:691:98//AC005666

F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), comp  
lete sequence.//6.0e-138:660:98//AC005600

F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), co  
mplete sequence.//0.066:333:60//AC003676

F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial c  
ds.//1.1e-39:404:74//AF068748

F-MAMMA1002269//HS\_3163\_B1\_D03\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3163 Col=5 Row=H, genomic survey s  
equence.//1.0:150:63//AQ171576

F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327024, complete  
sequence.//1.5e-22:315:67//AC003108

F-MAMMA1002292//B.garinii (strain TIs1) p83/100 gene (partial).//0.73:20  
0:64//X81533

F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25  
unordered pieces.//1.6e-56:408:75//AC006023

F-MAMMA1002294//Sequence 2 from Patent W09516779.//1.8e-06:401:62//A4525

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F-MAMMA1002297

F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:525:61//AC004221

F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey sequence.//1.2e-90:446:98//AQ053994

F-MAMMA1002308//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.3e-35:329:78//AL031680

F-MAMMA1002310//Human gastric (H+ + K+)-ATPase gene, complete cds.//0.0060:301:60//J05451

F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737

F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome X q25. Contains ESTs and STS.//1.3e-09:741:58//Z86064

F-MAMMA1002317

F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//AC005756

F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//5.3e-52:617:70//AC004796

F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//U93871

F-MAMMA1002332//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//1.6e-31:287:74//AL034402

F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//2.5e-09:674:59//AL022022

F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases 1..41604.//2.1e-57:522:77//AJ011932

F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete



sequence.//2.0e-14:258:69//AC004129

F-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORKING DRAFT SEQUENCE.//7.8e-132:723:91//AL022100

F-MAMMA1002352//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 12803, WORKING DRAFT SEQUENCE.//5.8e-17:326:70//Z98742

F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.1e-14:399:63//AC004825

F-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING DRAFT SEQUENCE.//3.7e-43:420:75//AL023879

F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153

F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.3e-18:156:75//AC005831

F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.//4.9e-43:353:69//Z68885

F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//1.8e-22:282:74//AL008719

F-MAMMA1002362//Platemys spixii CR1-like LINE, partial sequence.//0.00058:83:79//D82938

F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey sequence.//4.4e-10:85:92//AQ196889

F-MAMMA1002384//RPCI11-80J20.TV RPCI11 Homo sapiens genomic clone R-80J20, genomic survey sequence.//2.7e-56:286:98//AQ284134

F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey sequence.//5.5e-46:335:84//AQ043985

F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete seq

uence.//8.5e-29:273:78//AC004888

F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL0238

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F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//9.6e-08:730:57//L40608

F-MAMMA1002417//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402

F-MAMMA1002427//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604

F-MAMMA1002428

F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z9302

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F-MAMMA1002446//CIT-HSP-2324022.TR CIT-HSP Homo sapiens genomic clone 2324022, genomic survey sequence.//2.3e-56:302:95//AQ027479

F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229

F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005

F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556

F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC00467

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F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.025:100:76//AC005077

F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.

//2.9e-118:560:98//AF055460

F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome System s Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913

F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-10:330:64//AC002477

F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.4e-160:775:97//AF065214

F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//1.9e-41:345:80//AC005696

F-MAMMA1002554

F-MAMMA1002556

F-MAMMA1002566

F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 22 96N17, genomic survey sequence.//1.7e-07:76:90//AQ006579

F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GA A C27.//2.7e-08:195:70//AB018507

F-MAMMA1002585

F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.//2.1e-26:361:69//AC005019

F-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548

F-MAMMA1002598//H.sapiens mRNA for ribosomal protein L7.//1.1e-21:123:100//X57958

F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//0.0018:358:61//AC005220

F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336:63//AC004861

F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229:64//AC005486

F-MAMMA1002618

F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.5e-7 1:319:85//AJ010598

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-20:157:90//AF041449

F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from base s 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence. //8.3e-06:137:72//AE000660

F-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING DRAFT SEQUENCE.//1.9e-171:819:98//AL031727

F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence.//4.8e-85:478:78//AC003093

F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds.//5.6e-09:499:62//U10063

F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//3.6e-115:785:82//AF055666

F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.5e-45:291:90//AC002038

F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds.//6.6e-06:661:59//L41919

F-MAMMA1002655//HS\_2003\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2003 Col=22 Row=A, genomic survey sequence.//9.0e-15:198:74//AQ224233

F-MAMMA1002662

F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.4e-37:235:84//AC005029

F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.//

0.00027:272:64//U22398

F-MAMMA1002673

F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//3  
.7e-161:752:99//D86987

F-MAMMA1002685//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 394I7, WORKING DRAFT SEQUENCE.//6.2e-45:510:70//AL023585

F-MAMMA1002698//HS\_3024\_B1\_C06\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3024 Col=11 Row=F, genomic survey  
sequence.//1.7e-10:155:75//AQ072214

F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA,  
complete cds.//5.9e-75:509:83//AF018261

F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//1.2e-159:749:  
99//AB011399

F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.  
2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs an  
d GSSs, complete sequence.//3.0e-57:347:79//AL031053

F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete  
sequence.//3.4e-31:484:69//AC005030

F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 235  
0M5, genomic survey sequence.//1.4e-06:265:63//AQ061245

F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1  
-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-bin  
ding Protein 2, and a possible pseudogene in an intron of this gene. Con  
tains STSs and GSSs and an AAAT repeat polymorphism, complete sequence./  
/0.18:386:58//AL023584

F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X conta  
ins cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-amin  
olevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructos  
e-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//3.2e-05

:362:63//Z83821

F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//0.00010:535:58//AE001368

F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.2e-182:880:97//AC005856

F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-175:829:98//AC006055

F-MAMMA1002754//Homo Sapiens Chromosome X clone bWxD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.1e-31:372:75//AC004676

F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98//AB007902

F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence.//5.2e-49:355:81//U73636

F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey sequence.//6.7e-13:155:76//B92153

F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey sequence.//9.7e-21:151:90//AQ028244

F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//5.6e-105:179:99//U07561

F-MAMMA1002780//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-08, complete sequence.//0.071:277:58//Z98546

F-MAMMA1002782//HS\_3213\_B2\_B08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=16 Row=D, genomic survey sequence.//0.00018:219:63//AQ175845

F-MAMMA1002796

F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; complete sequence.//6.9e-22:332:69//AC002404

F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Pa

rk Cancer Institute Human PAC Library) complete sequence.//5.9e-11:483:62//AC003035

F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//1.0e-64:320:83//AC002553

F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//2.8e-47:413:80//AC004875

F-MAMMA1002835

F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence.//1.1e-39:164:83//B14462

F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//1.9e-62:373:81//U58883

F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.7e-135:635:99//AB018353

F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence.//6.7e-17:383:66//B11616

F-MAMMA1002858

F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence.//8.3e-81:392:99//AQ081566

F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//I25863

F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.029:370:59//L12388

F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518

F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds.//1.2e-28:680:61//D45027

F-MAMMA1002886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653

F-MAMMA1002887//HS\_3238\_B2\_G08\_MR CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence.//5.5e-79:401:97//AQ219814

F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes.//4.6e-35:136:73//AF109906

F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//5.7e-14:450:60//AC004096

F-MAMMA1002895//H.sapiens CpG island DNA genomic MseI fragment, clone 46 b6, forward read cpg46b6.ft1a.//3.7e-36:190:100//Z58616

F-MAMMA1002908//Penaeus monodon microsatellite locus Pmo27.//1.1e-05:195:62//AF068828

F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1.0e-13:457:61//AC002402

F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human BAC library) complete sequence.//0.25:260:62//AC004467

F-MAMMA1002937//H.sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623

F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds.//5.1e-193:910:98//AB014598

F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCR L2-GGT Region, complete sequence.//2.7e-23:174:77//AC004032

F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome.//1.3e-09:475:61//AF010496

F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5.//0.0029:314:60//AF019366

F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RSL gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//4.0e-10:194:71//Z94056



F-MAMMA1002972//H.sapiens CpG island DNA genomic MseI fragment, clone 2g 10, forward read cpg2g10.ft1aa.//0.38:156:66//Z55272

F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//2.9e-41:234:79//AC005919

F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6 p24.1-p25.3.//1.7e-05:322:63//AL022098

F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence.//0.0064:135:66//AQ275871

F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence.//2.8e-31:201:89//B01998

F-MAMMA1003004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y237C10, WORKING DRAFT SEQUENCE.//1.6e-10:180:73//AL031601

F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus.//3.5e-12:435:61//L04732

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//2.3e-50:734:67//U79139

F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.2e-86:341:79//AC003694

F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence.//2.6e-13:443:61//AC003661

F-MAMMA1003019//HS\_3221\_A1\_A01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=1 Row=A, genomic survey sequence.//2.8e-51:299:92//AQ184271

F-MAMMA1003026

F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//0.0037:134:73//AC005214

F-MAMMA1003035//RPCI11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey sequence.//1.1e-07:66:100//B74936

F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.1e-19:220:76//AC004671

F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36. 2. Contains ESTs, polymorphic CA repeat, trna and endogenous retrovirus. //9.5e-91:469:78//Z98257

F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11. 2-12.3 Contains EST, GSS, complete sequence.//0.21:289:61//AL031321

F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//1.7e-139:663:98//AF077952

F-MAMMA1003049

F-MAMMA1003055//HS\_3014\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=20 Row=L, genomic survey sequence.//4.2e-05:215:64//AQ164940

F-MAMMA1003056//HS\_3221\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=24 Row=H, genomic survey sequence.//1.4e-16:206:74//AQ302772

F-MAMMA1003057//M.domesticus MD6 mRNA.//8.5e-128:654:94//X54352

F-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING DRAFT SEQUENCE.//1.0:142:71//AL034371

F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.7e-42:373:78//AC004796

F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6e-42:288:88//AF042166

F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//1.6e-12:477:64//U72634

F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//3.4e-121:789:85//AF071316

F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain.//9.4e-5

8:423:83//X68199

F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP)  
mRNA, complete cds.//0.62:676:58//U67916

F-MAMMA1003140

F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//2.2e-80:397:97//Y1  
5062

F-MAMMA1003150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 598F2, WORKING DRAFT SEQUENCE.//7.3e-123:266:88//AL021579

F-MAMMA1003166//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 250D10, WORKING DRAFT SEQUENCE.//1.6e-33:143:82//Z99716

F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.  
1-21.33. Contains GSSs, complete sequence.//0.50:216:61//Z95400

F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-65:385:  
92//D31886

F-NT2RM1000032

F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SC  
AP) mRNA, complete cds.//6.3e-135:565:84//U67060

F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.  
1e-106:542:95//AB014590

F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0.080:239:60//L2  
7155

F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//8.4e-9  
6:535:91//D87671

F-NT2RM1000059//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600

F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene,  
partial cds.//0.54:306:63//U37520

F-NT2RM1000080//Sequence 2 from patent US 5763589.//1.5e-115:566:97//AR0  
12692

F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//1  
.8e-114:550:97//AB014561

F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequ  
ence.//0.63:180:65//AC005594

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.0  
27:126:70//AF007155

F-NT2RM1000119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 466N1, WORKING DRAFT SEQUENCE.//0.022:644:58//Z97630

F-NT2RM1000127//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5,  
genomic survey sequence.//1.6e-45:254:94//AQ195884

F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds.//5  
.5e-153:778:95//AB018335

F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subun  
it mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1  
e-90:448:97//AF044959

F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequen  
ce.//5.9e-07:66:96//U49890

F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.0  
25:126:70//AF007155

F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2  
510J4, genomic survey sequence.//1.1e-05:56:98//AQ261184

F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 pre  
cursor, complete cds.//1.6e-38:711:65//D64009

F-NT2RM1000242

F-NT2RM1000244//HS\_2229\_A1\_C04\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2229 Col=7 Row=E, genomic survey s  
equence.//2.0e-13:95:95//AQ298474

F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206\_C\_20, complet  
e sequence.//0.023:225:61//AC006070

F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence./  
/8.5e-24:473:64//Z68336  
F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds.//6.4e-69:455:85//  
AF035940  
F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds.//6.5e-57:460  
:80//D50920  
F-NT2RM1000271  
F-NT2RM1000272  
F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, comp  
lete cds.//6.7e-97:430:92//U11927  
F-NT2RM1000300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 92N15, WORKING DRAFT SEQUENCE.//2.1e-96:170:100//Z93097  
F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e-127:70  
8:92//D63880  
F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cd  
s.//5.7e-34:182:99//D79205  
F-NT2RM1000341//Homo sapiens full length insert cDNA clone YP11F06.//1.3  
e-100:504:97//AF085879  
F-NT2RM1000354//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey  
sequence.//1.6e-11:201:73//AQ218494  
F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds.//1.8e-77:5  
78:82//U76253  
F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//9.4e-113:367:97//AC004821  
F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4.//6.1e-14:36  
2:62//Y08302  
F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, c  
omplete cds.//1.0:482:58//U26679

F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z85979

F-NT2RM1000399

F-NT2RM1000421//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-08:195:72//AQ032737

F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928

F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525:69//D79989

F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//4.6e-73:533:83//AC004993

F-NT2RM1000553

F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:555:97//AF070542

F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-123:477:100//AC004873

F-NT2RM1000623//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//8.2e-06:75:89//AQ032737

F-NT2RM1000648//Halobium cutirubrum L11, L1, L10 and L12 equivalent ribosomal protein gene cluster.//1.3e-06:414:61//X15078

F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds.//9.3e-54:275:97//AF047695

F-NT2RM1000666//HS\_2016\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-13:199:73//AQ227865

F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323

and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSS, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133

F-NT2RM1000672

F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582:98//AB015348

F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627

F-NT2RM1000702//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208

F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//0.92:395:58//AJ011930

F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds.//2.1e-70:407:92//L39210

F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.6e-36:98:93//AC000380

F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:126:99//X52233

F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//

AC004153

F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z  
97207

F-NT2RM1000802

F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:  
490:84//AF027208

F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96/  
/AF070542

F-NT2RM1000829//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey s  
equence.//0.74:215:67//AQ099134

F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds.//5.  
1e-114:683:88//M96629

F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic surve  
y sequence.//1.1e-26:279:74//AL018762

F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partia  
l.//9.3e-148:726:97//AJ010840

F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exo  
n 2.//0.97:124:65//AB008378

F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA  
143D.//1.2e-31:172:98//X95834

F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds.//2.8e-131:  
632:97//AF064605

F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 cont  
aining human gene for ferritin heavy chain (FTH), complete sequence.//1.  
2e-98:214:99//AC004228

F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, comple  
te cds.//2.7e-156:762:97//AF082516

F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2



.0e-17:310:67//AB014561

F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//3.2e-95:469:83//U58280

F-NT2RM1000898

F-NT2RM1000905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//1.8e-74:188:98//Z97630

F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:601:98//AC004873

F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.071:392:60//AC004846

F-NT2RM1000962//H.sapiens CpG island DNA genomic MseI fragment, clone 140d1, forward read cpg140d1.ft1a.//4.1e-35:187:99//Z56803

F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-23:266:77//AC005959

F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//4.0e-160:760:98//U97067

F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//1.7e-11:602:61//U52064

F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125

F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL022245

F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.//3.8e-53:261:80//AC005915

F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.64:285:59//B94391

F-NT2RM1001072//HS\_3115\_B1\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey

sequence.//7.3e-23:140:95//AQ147905  
 F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//AC005263  
 F-NT2RM1001082//Sequence 1 from Patent W09718303.//2.1e-144:736:95//A62731  
 F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence.//8.8e-45:235:97//AQ020757  
 F-NT2RM1001092//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489  
 F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964  
 F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5' UTR).//0.0014:349:61//Z95973  
 F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//AC004678  
 F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624  
 F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//AC004755  
 F-NT2RM2000006//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291  
 F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826  
 F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//AC004863  
 F-NT2RM2000032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379  
 F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418

F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269

F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//0.38:312:62//AF109905

F-NT2RM2000101

F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds.//3.8e-58:297:97//M12303

F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224

F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//2.2e-33:191:95//B93289

F-NT2RM2000239//F.rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//AL018549

F-nnnnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292

F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162

F-NT2RM2000259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310013, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658

F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934

F-NT2RM2000287//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656

F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-

25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864

F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132

F-NT2RM2000363//RPCI11-90B10.TJ RPCI11 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300

F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251

F-NT2RM2000371//RPCI11-57I4.TJ RPCI11 Homo sapiens genomic clone R-57I4, genomic survey sequence.//1.1e-52:312:91//AQ083343

F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514

F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99:345:58//AE001274

F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973

F-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//1.4e-131:439:88//AF030430

F-NT2RM2000420//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Spermlibrary D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204

F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022

F-NT2RM2000452//HS\_3009\_B2\_D05\_MR CIT Approved Human Genomic Spermlibrary D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794

F-NT2RM2000469//HS\_2019\_A1\_G02\_MR CIT Approved Human Genomic Spermlibrary D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey s

equence.//9.6e-22:176:85//AQ229041

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.  
5e-15:386:63//AB018290

F-NT2RM2000502

F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.  
//5.1e-171:824:97//AF061243

F-NT2RM2000522

F-NT2RM2000540

F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Can  
cer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC0  
04466

F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-  
154:751:97//AF072132

F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial  
cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown  
gene.//3.0e-06:664:58//AF083252

F-NT2RM2000569//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681

F-NT2RM2000577//RPCI11-43G22.TJ RPCI11 Homo sapiens genomic clone R-43G2  
2, genomic survey sequence.//1.6e-14:155:80//AQ199391

F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5  
.4e-174:820:98//D86987

F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Can  
cer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC0  
04466

F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3  
b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626

F-NT2RM2000599//O.sativa osr40g3 gene.//0.30:585:56//Y08988

F-NT2RM2000609

F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776

F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952

F-NT2RM2000624

2.9e-06:231:64//Z82061

F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272

F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558

F-NT2RM2000639//RPCI11-69E5.TJ RPCI11 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491

F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576

F-NT2RM2000669

F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038

F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984

F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342

F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244

F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691

F-NT2RM2000795//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING DRAFT SEQUENCE.//1.0e-78:723:76//AL021392

F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228

F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361:62//AC005017

F-NT2RM2000951//Homo sapiens XYLb mRNA for xylulokinase, complete cds.//  
8.7e-184:847:99//AB015046

F-NT2RM2000952

F-NT2RM2000984//Mus musculus major histocompatibility locus class III re  
gions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG  
24, NG25, and NG26 genes, complete cds; and unknown genes.//7.6e-41:239:  
76//AF109905

F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 23  
33N18, genomic survey sequence.//1.1e-11:298:66//AQ035862

F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120  
:627:91//U21855

F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, comple  
te cds.//6.8e-118:690:88//AF071314

F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//2.3e-145:614:99//AC004873

F-NT2RM2001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 50024, WORKING DRAFT SEQUENCE.//2.7e-95:461:99//AL034380

F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homo  
log gene, complete cds.//7.2e-24:726:62//U52064

F-NT2RM2001141

F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq  
21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort prot  
ein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Chor  
oideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains E  
STs and an STS, complete sequence.//0.98:300:62//AL022401

F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15  
unordered pieces.//1.2e-147:741:96//AC005488

F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 ge  
nes, complete cds, UL8 gene, partial cds.//0.026:408:59//U66829

F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-135:627:98//AC004987

F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700

F-NT2RM2001221//Chimpanzee (P.paniscus) involucrin, complete cds.//0.53:670:55//M26514

F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150

F-NT2RM2001243

F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey sequence.//0.0011:274:59//AQ276184

F-NT2RM2001256//M.musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169

F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey sequence.//4.6e-09:156:72//B57734

F-NT2RM2001306//RPCI11-28I5.TP RPCI-11 Homo sapiens genomic clone RPCI-11-28I5, genomic survey sequence.//0.069:234:64//B84850

F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.1e-22:111:81//AC005919

F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:58//AE001118

F-NT2RM2001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 209H1, WORKING DRAFT SEQUENCE.//3.7e-44:340:85//Z84465

F-NT2RM2001345//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290:58//AQ089514

F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365:87//U56429

F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete



sequence.//0.98:415:58//AC004899  
F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2  
-GGT Region, complete sequence.//4.0e-54:394:75//AC004033  
F-NT2RM2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520  
F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1  
e-96:453:99//AJ007509  
F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transport  
er 3, complete cds.//7.1e-91:601:83//AB000113  
F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequ  
ence.//0.81:200:69//AC005624  
F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig  
fragment No. 2.//3.8e-16:316:65//Z99708  
F-NT2RM2001544  
F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.  
//3.3e-24:318:67//AL032657  
F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.  
//2.1e-26:582:64//M34551  
F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750  
F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65  
//AB007902  
F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:7  
36:90//AF032667  
F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre  
-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431  
F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-  
118:779:85//M96630  
F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete  
sequence.//1.5e-50:561:71//AC004691

F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9  
.2e-153:740:98//AB014518  
F-NT2RM2001637//F.rubripes GSS sequence, clone 155D22bD8, genomic survey  
sequence.//2.5e-13:224:64//Z91020  
F-NT2RM2001641//CIT-HSP-2347F23.TF CIT-HSP Homo sapiens genomic clone 23  
47F23, genomic survey sequence.//1.3e-67:340:98//AQ060913  
F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.  
4e-110:459:89//M96629  
F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1  
) mRNA, complete cds.//1.2e-153:807:93//AF023451  
F-NT2RM2001659//nbxb0002cE07f CUGI Rice BAC Library Oryza sativa genomic  
clone nbxb0002J13f, genomic survey sequence.//1.0:485:56//AQ051653  
F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP)  
mRNA, complete cds.//3.7e-172:802:99//AF044195  
F-NT2RM2001668  
F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070  
and D16S3275, containing Familial Mediterranean Fever gene disease.//3.2  
e-18:279:70//AJ003147  
F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 m  
RNA, complete cds.//1.6e-137:683:94//U21157  
F-NT2RM2001675//RPCI11-51J16.TJ RPCI11 Homo sapiens genomic clone R-51J1  
6, genomic survey sequence.//1.0:394:58//AQ053677  
F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T805 (E  
SSAII project).//0.87:220:61//AL021890  
F-NT2RM2001688//B.parapertussis bvg locus (transcription regulators of v  
irulence factors) with bvgA and bvgS genes.//1.0:286:62//X52948  
F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 34  
5H13, genomic survey sequence.//3.2e-53:241:82//B59854  
F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, cl

one Mu2.//1.2e-05:306:58//M10668

F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1 p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:59//AL021920

F-NT2RM2001699//HS\_3195\_B2\_D01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, genomic survey sequence.//2.7e-07:322:61//AQ189056

F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.//7.8e-05:354:58//Z95556

F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//7.5e-42:335:81//AC004469

F-NT2RM2001716

F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//4.2e-08:536:58//AC004290

F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:163:95//AF052123

F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//6.2e-111:530:98//AB007931

F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//3.1e-102:248:95//AJ010598

F-NT2RM2001743

F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.11:138:66//Z68117

F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds.//9.4e-100:418:88//M96629

F-NT2RM2001768//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993

F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323),

complete sequence.//1.3e-66:680:72//AC006116

F-NT2RM2001782

F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//0.027:384:60//Z48053

F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770

F-NT2RM2001797//HS\_3045\_A1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, genomic survey sequence.//1.4e-74:381:97//AQ129456

F-NT2RM2001800

F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195

F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR.//1.0:290:58//AF053126

F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//3.3e-16:109:95//B89870

F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-131:738:90//AF013759

F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//AC002347

F-NT2RM2001855//HS\_3224\_A1\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=0, genomic survey sequence.//0.00012:68:91//AQ205285

F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene

and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSS, GSSs and a putative CpG island, complete sequence.//0.068:102:70//AL031177

F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers DXS366 and DXS87 on chromosome X.//0.0029:500:59//Z68328

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610

F-NT2RM2001896//S.cerevisiae chromosome III complete DNA sequence.//8.6e-30:613:63//X59720

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.9e-176:859:97//AB007931

F-NT2RM2001930//M.musculus mRNA for semaphorin G.//4.7e-117:730:85//X97818

F-NT2RM2001935//Sequence 11 from Patent WO9610637.//1.0:356:60//A50028

F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence.//6.9e-138:653:98//AF091080

F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700

F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.//0.42:179:65//AC005825

F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//3.8e-20:123:98//AF089816

F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981

F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5.//9.6e-25:160:95//D16955

F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151

F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//  
AC002407

F-NT2RM2002014

F-NT2RM2002030//Mus musculus glutamine:fructose-6-phosphate amidotransfe  
rase mRNA, complete cds.//1.5e-89:822:74//U00932

F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M2613  
2

F-NT2RM2002055

F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial  
sequence.//1.4e-15:421:63//AF073936

F-NT2RM2002091//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 50024, WORKING DRAFT SEQUENCE.//4.6e-160:771:98//AL034380

F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partia  
l.//7.7e-164:776:98//AJ010840

F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (G  
AC1) mRNA, complete cds.//2.4e-143:684:98//AF030435

F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein  
beta 5 (Gnb5) mRNA, complete cds.//7.0e-27:330:73//U13152

F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete c  
ds.//6.3e-10:135:80//U27121

F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, c  
omplete cds.//4.2e-143:800:92//AF084928

F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.  
2e-164:787:97//AB007936

F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147))  
, complete sequence.//7.4e-13:337:62//AC004423

F-NT2RM4000024//D.melanogaster DmRP128 gene for RNA polymerase III secon  
d-largest subunit.//1.2e-62:801:70//X58826

F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336:60//U3742

9

F-NT2RM4000030//H.sapiens CpG island DNA genomic MseI fragment, clone 56 h10, forward read cpg56h10.ft1a.//9.3e-22:127:100//Z55685

F-NT2RM4000046//Curcubita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059

F-NT2RM4000061

F-NT2RM4000085//B.taurus mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829

F-NT2RM4000086

F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//4.2e-23:345:69//AF060865

F-NT2RM4000139//R.norvegicus trg mRNA.//1.4e-56:708:69//X68101

F-NT2RM4000155//CIT-HSP-2282N15.TR CIT-HSP Homo sapiens genomic clone 22 82N15, genomic survey sequence.//3.0e-09:88:90//AQ000070

F-NT2RM4000156//H.sapiens HPBR11-7 gene.//2.0e-21:586:60//X67336

F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:90//D12646

F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//A C004157

F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:60//AF051726

F-NT2RM4000197

F-NT2RM4000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//0.67:461:60//AL031667

F-NT2RM4000200

F-NT2RM4000202//H.sapiens CpG island DNA genomic MseI fragment, clone 34 c2, forward read cpg34c2.ft1a.//1.7e-27:190:90//Z65361

F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1

.4e-182:856:98//AB018255

F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:62//J03852

F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//4.6e-102:233:94//AC005383

F-NT2RM4000233//Mus musculus semaphorin VIA mRNA, complete cds.//1.6e-135:835:86//AF030430

F-NT2RM4000244//RPCI11-24P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P15, genomic survey sequence.//5.5e-08:422:62//B86757

F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//0.98:207:60//AC005855

F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone pDJ1081b4 containing human mRNA for T-cell glycoprotein CD6, complete sequence.//5.2e-41:707:65//AC003689

F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609:93//M99438

F-NT2RM4000324

F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//3.9e-44:727:68//AF022085

F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds.//1.0e-143:801:90//AF090430

F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700

F-NT2RM4000354//HS\_2221\_A2\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence.//1.0e-20:180:83//AQ253449

F-NT2RM4000356

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//1.6e-133:628:99//AB014542



F-NT2RM4000368//RPCI11-91B5.TJ RPCI11 Homo sapiens genomic clone R-91B5,  
genomic survey sequence.//5.0e-12:431:61//AQ283217  
F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds.//7.4e-86:84  
5:72//AF059485  
F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965.//2.5  
e-34:767:61//D44597  
F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//  
1.5e-15:114:94//AB015046  
F-NT2RM4000421  
F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complet  
e sequence.//1.5e-37:295:82//AC005921  
F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mR  
NA, complete cds.//3.9e-94:740:78//AF062476  
F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 23  
46B17, genomic survey sequence.//1.5e-22:149:92//AQ062111  
F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, pa  
rtial.//1.3e-76:386:97//AJ010952  
F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A,./1.1e-  
22:356:67//AB000459  
F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Can  
cer Institute Human BAC Library) complete sequence.//0.53:198:70//AC0059  
08  
F-NT2RM4000511  
F-NT2RM4000514  
F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 228  
5L3, genomic survey sequence.//0.0012:200:66//AQ000113  
F-NT2RM4000520  
F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.  
//2.9e-31:732:64//M58297

F-NT2RM4000532//HS\_3231\_B1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-59:362:90//AQ192093

F-NT2RM4000534

F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone 2508I18, genomic survey sequence.//1.1e-34:208:93//AQ260706

F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence.//8.3e-34:180:99//AQ004125

F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//1.2e-09:203:66//AC005288

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:68//AB002390

F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870

F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase.//2.3e-59:721:68//Z46786

F-NT2RM4000674

F-NT2RM4000689//CIT-HSP-2381013.TF CIT-HSP Homo sapiens genomic clone 2381013, genomic survey sequence.//2.6e-31:174:97//AQ110303

F-NT2RM4000698

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789

F-NT2RM4000717

F-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018303

F-NT2RM4000741

F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593

F-NT2RM4000764

F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790

F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920

F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-qter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRFS1) exon, ESTs, STS, CA repeat and CpG island.//0.0057:163:69//Z82206

F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//AC005306

F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA, complete cds.//5.9e-97:857:74//U41663

F-NT2RM4000796//HS\_3214\_B1\_F11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988

F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//6.2e-78:816:72//AF023451

F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109

F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406

F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373

F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.0:477:56//AC005940

F-NT2RM4000852

F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete

e sequence.//3.4e-29:229:83//AC003957

F-NT2RM4000887

F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004

F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.//0.41:311:64//AC004929

F-NT2RM4000971//RPCI11-53H3.TJ RPCI11 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735

F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.3e-19:207:78//AC005245

F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651

F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272

F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539

F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276

F-NT2RM4001047//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858

F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629

F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479

F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776

F-NT2RM4001116

F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete

sequence.//1.9e-136:717:93//AC004593

F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-ORF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249

F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706

F-NT2RM4001160

F-NT2RM4001187

F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence.//6.2e-12:181:72//B53378

F-NT2RM4001200//H.sapiens HZF10 mRNA for zinc finger protein.//1.3e-66:799:69//X78933

F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//4.2e-152:707:99//AF004828

F-NT2RM4001204

F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.//1.6e-62:715:70//AF005381

F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884

F-NT2RM4001258//HS\_3171\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=18 Row=N, genomic survey sequence.//2.5e-18:215:77//AQ149676

F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163

F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973

F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U97002

F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016

F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127

F-NT2RM4001344//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y1E3, WORKING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388

F-NT2RM4001347

F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786

F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799

F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 2 2q12.1. Contains ESTs, STSS and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393

F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//0.027:336:58//AP000023

F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//5.9e-124:783:85//AF020526

F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183

F-NT2RM4001414//Homo sapiens full length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563

F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-47:623:69//AC004226

F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH),

cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901

F-NT2RM4001454

F-NT2RM4001455

F-NT2RM4001483//Human zinc finger protein ZNF136.//3.2e-36:329:78//U09367

F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//1.2e-155:724:99//AB014585

F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00019:418:59//AC004688

F-NT2RM4001522//Human HepG2 3' region MboI cDNA, clone hmd6a08m3.//1.4e-16:130:88//D17274

F-NT2RM4001557

F-NT2RM4001565

F-NT2RM4001566

F-NT2RM4001569//HS\_2050\_B1\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2050 Col=15 Row=F, genomic survey sequence.//2.7e-09:109:84//AQ234720

F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//AF071317

F-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1.//7.3e-117:710:88//X69942

F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered pieces.//0.34:388:59//AC002355

F-NT2RM4001597//M.musculus red-1 gene.//6.2e-139:788:90//X92750

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//3.3e-162:750:99//AB018334

F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27, 143041

9-1576592.//2.5e-05:490:58//D90910

F-NT2RM4001629//Mus musculus palmytoylated protein p55 mRNA, complete cds.//0.65:186:64//U38196

F-NT2RM4001650//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0435P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.99:422:59//AC004689

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds.//2.6e-81:449:93//AB002320

F-NT2RM4001666

F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence.//3.2e-35:240:87//AF046699

F-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//1.9e-151:564:97//AL031447

F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds.//7.0e-85:748:74//D86957

F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.2e-91:488:94//AL034430

F-NT2RM4001731//Orang-utan involucrin gene, complete cds.//0.40:530:59//M25312

F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123

F-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING DRAFT SEQUENCE.//2.3e-49:320:89//AL031709

F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//6.3e-64:379:76//AC005831

F-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//3.7e-146:871:87//Z83868

F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270



F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//2.0e-1  
65:593:99//AC006017

F-NT2RM4001810

F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 from 2, complete sequen  
ce.//7.1e-31:176:84//AC005036

F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein  
kinase) mRNA, complete cds.//4.4e-34:195:95//M37712

F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete  
cds.//3.3e-51:490:75//U49046

F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRN  
A, complete cds.//5.6e-74:688:72//U28687

F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR  
Region, complete sequence.//1.0:406:60//AC000076

F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alt  
ernatively spliced isoform 2, complete cds.//1.6e-131:831:86//AF033275

F-NT2RM4001842//HS\_3163\_A2\_G10\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3163 Col=20 Row=M, genomic survey  
sequence.//1.5e-05:355:60//AQ168513

F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U  
70855

F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds.//6.  
4e-11:266:66//U64433

F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//6  
.9e-149:704:98//Y17711

F-NT2RM4001876//F.rubripes GSS sequence, clone 060E22ba4, genomic survey  
sequence.//5.7e-48:600:68//Z88651

F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 234  
8J1, genomic survey sequence.//0.0025:61:88//AQ060809

F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:5

35:67//X98335

F-NT2RM4001922//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732

F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MXI10, complete sequence.//4.9e-10:269:63//AB005248

F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//7.6e-152:311:100//AC005207

F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162

F-NT2RM4001953//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4 , BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:86//AC004046

F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 11/11 .//1.6e-107:622:90//AB020868

F-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99330

F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341

F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:502:60//Z82253

F-NT2RM4001987//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//2.6e-33:177:99//AQ051701

F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//0.019:65:90//AC005921

F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.//1.0:527:57//L15344

F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq2

6.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712

F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//U01882

F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-44:473:76//AC005283

F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540

F-NT2RM4002062//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3 ; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:298:59//AC005122

F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//U82267

F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783

F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//1.1e-53:295:76//AC005216

F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:277:75//AF072758

F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.0e-23:588:61//AF059569

F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:69//X60789

F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4 , complete cds.//2.0e-121:762:86//D12646

F-NT2RM4002128//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312

F-NT2RM4002140

F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//1.8e-49:736:65//AC004152

F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//AF035940

F-NT2RM4002161//Homo sapiens mRNA for LAFPTase, isoform 1, partial.//4.2e-151:763:96//AJ130763

F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome.//2.1e-16:580:60//AE000540

F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 2 2q13.2-13.33. Contains ESTs.//1.0e-07:792:61//AL008636

F-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//3.2e-132:782:87//AF030430

F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//1.5e-40:292:84//L14684

F-NT2RM4002213

F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160

F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//AC004448

F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959

F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006I18aG12, genomic survey sequence.//3.3e-12:217:67//AL024779

F-NT2RM4002278//HS\_3089\_A1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653

F-NT2RM4002281

F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515

F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457

F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881

F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudogene similar to GPISG20 and other exonucleases). Contains ESTs, STSSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822

F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865

F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849

F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549

F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC library) complete sequence.//0.00040:312:63//AC002978

F-NT2RM4002383//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284

F-NT2RM4002390

F-NT2RM4002398//CIT-HSP-2288N22.TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence.//3.4e-35:184:100//AQ001110

F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-16:468:59//AE001092

F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336

F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from

the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands, ./9.6e-64:467:84//Z92845

F-NT2RM4002452

F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence. ./2.2e-24:201:86//Z85988

F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence. ./1.3e-45:487:70//AC004690

F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds. ./2.7e-163:777:98//AF083255

F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds. ./2.3e-93:464:97//AB014591

F-NT2RM4002493

F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces. ./3.5e-41:442:75//AC005484

F-NT2RM4002504//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence. ./3.8e-31:233:87//AL031577

F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence. ./7.7e-08:274:62//AL027162

F-NT2RM4002532

F-NT2RM4002534

F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds. ./3.8e-53:394:81//AF072759

F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds. ./6.4e-160:902:89//AF022962

F-NT2RM4002567//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence. ./8.5e-31:220:88//AQ263402

F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 mRNA, complete cds. ./5.2e-05:199:65//AF049344

F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875

F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454

F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122

F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385

F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//1.1e-153:747:96//AJ012449

F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047

F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784

F-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//2.8e-183:548:91//X98834

F-NT2RP1000101//H.sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.ft1a.//6.0e-27:163:95//Z60555

F-NT2RP1000111//CIT-HSP-2307014.TR CIT-HSP Homo sapiens genomic clone 2307014, genomic survey sequence.//1.2e-11:128:81//AQ016069

F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:324:81//M86699

F-NT2RP1000124//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557

F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:68//E08546

F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//6.7e-05:77:90//AF011792

F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.9e-20:431:64//AC006030

F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence.//2.5e-138:679:97 //AF070535

F-NT2RP1000191

F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds.//5.3e-05:220:61//D89496

F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//4.7e-51:508:69//AC004373

F-NT2RP1000259

F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds.//7.8e-142:866:88//AF042383

F-NT2RP1000324//RPCI11-81021.TJ RPCI11 Homo sapiens genomic clone R-81021, genomic survey sequence.//2.8e-29:182:92//AQ285136

F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//4.2e-147:693:98//AF053551

F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence.//1.4e-08:281:61//Z75525

F-NT2RP1000348//H.sapiens CpG island DNA genomic MseI fragment, clone 12 f1, reverse read cpg12f1.rtlc.//1.7e-09:71:100//Z56610

F-NT2RP1000357

F-NT2RP1000358

5.7e-16:403:61//AC005456

F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.8e-125:497:86//AB014538

F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds.//1.8e-176:877:96//AF064594

F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp.//4.6e-106:700:84//AJ001558



F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9  
.4e-178:710:98//AB011159

F-NT2RP1000416

F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3  
' end of cds.//1.0:198:60//L40178

F-NT2RP1000439//HS\_2182\_A1\_D06\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey  
sequence.//2.1e-68:441:87//AQ024305

F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18  
/28, WORKING DRAFT SEQUENCE.//3.8e-57:185:88//AP000047

F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete  
sequence.//2.7e-132:204:99//AC004453

F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, gen  
omic sequence, complete sequence.//4.9e-80:196:95//AC002985

F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, comp  
lete cds.//1.9e-55:440:80//U47634

F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome  
1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronection,  
Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S rib  
osomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, g  
enomic marker D1S2691 and STSS.//2.6e-92:562:88//Z99297

F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2  
.0e-130:622:98//D87686

F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN g  
enes, complete cds's.//0.11:360:58//M81648

F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8  
unordered pieces.//4.9e-34:209:93//AC004895

F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein C  
Hop24 mRNA, partial cds.//1.2e-08:331:63//U26264

F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds.//4.4e-81:295:92//AF017418

F-NT2RP1000577//HS\_2228\_B2\_C05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence.//1.9e-31:179:75//AQ185128

F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620

F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770

F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419

F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete sequence.//1.0:203:63//Z85989

F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943

F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907

F-NT2RP1000695

F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//I30536

F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-19:188:81//AC004932

F-NT2RP1000730

F-NT2RP1000733//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:315:75//U95742

F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//8.0e-122:604:96//AF101434

F-NT2RP1000746//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=0, genomic survey s

equence.//1.5e-83:466:92//AQ186344

F-NT2RP1000767//Homo sapiens full length insert cDNA clone ZD81B04.//2.8e-21:144:91//AF086442

F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213

F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13.

Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244

F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837

F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020

F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398

F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//U96629

F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812

F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//6.7e-106:551:95//AF064094

F-NT2RP1000902//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 316D5, WORKING DRAFT SEQUENCE.//0.0097:55:100//Z82199

F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R).//1.3e-3  
0:174:97//Z94761

F-NT2RP1000916

F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon.//0.19:103:7  
2//L49362

F-NT2RP1000944//HS\_2179\_B2\_C12\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2179 Col=24 Row=F, genomic survey  
sequence.//0.032:140:63//AQ065269

F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, c  
omplete cds.//3.7e-53:461:78//U62483

F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cos  
mid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//0.0  
30:89:78//B01950

F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence./  
/3.9e-11:445:61//Z49068

F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequenc  
e.//3.3e-57:326:92//AC004263

F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:98//M60  
858

F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 23  
14B10, genomic survey sequence.//0.32:137:68//AQ017126

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//  
L13435

F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mei-41) gene  
, complete cds, and TH1 gene, partial cds.//1.3e-31:497:65//U34925

F-NT2RP1001013//HS\_3068\_B1\_B09\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3068 Col=17 Row=D, genomic survey

sequence.//1.0e-24:414:66//AQ127667

F-NT2RP1001014//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//0.00052:83:81//AQ304711

F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//1.3e-134:241:99//AC004686

F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993

F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267

F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938

F-NT2RP1001113

F-NT2RP1001173

F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:373:68//U79139

F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039

F-NT2RP1001199

F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508

F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//7.3e-50:128:99//AC002036

F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4.3e-91:344:93//AF029914

F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's.//0.54:292:63//L44140

F-NT2RP1001294

F-NT2RP1001302

F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750

F-NT2RP1001311//RPCI11-67014.TK RPCI11 Homo sapiens genomic clone R-67014, genomic survey sequence.//0.26:80:75//AQ239291

F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228

F-NT2RP1001361//B.taurus CI-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647

F-NT2RP1001385

F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316

F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878

F-NT2RP1001424

F-NT2RP1001432

F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149

F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737

F-NT2RP1001466//HS\_3006\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336

F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375

F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//4.0e-87:563:8

5//L11316

F-NT2RP1001494

F-NT2RP1001543//Drosophila melanogaster DNA sequence (P1 DS01142 (D148))  
 , complete sequence.//1.9e-27:387:67//AC004280

F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cd  
 s.//8.0e-63:314:98//AF054840

F-NT2RP1001569//Mus musculus signal recognition particle receptor beta s  
 ubunit mRNA, complete cds.//1.2e-68:514:81//U17343

F-NT2RP1001616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U90913

F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 205  
 9N5, genomic survey sequence.//2.4e-45:305:88//B69912

F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence./  
 /1.5e-135:685:96//AF091081

F-NT2RP2000006//HS\_3061\_B2\_C03\_MR CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey s  
 equence.//1.9e-17:394:67//AQ178856

F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:  
 68//AB002390

F-NT2RP2000008//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424

F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequ  
 ence.//1.4e-32:345:75//AC005066

F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic surve  
 y sequence.//5.0e-41:445:72//Z88655

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.  
 9e-76:383:97//AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homol  
 og (TID1) mRNA, complete cds.//2.4e-95:467:97//AF061749

F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 23

28J24, genomic survey sequence.//3.3e-39:236:91//AQ043092  
 F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-50:311:90//D78610  
 F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:66//AF059485  
 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//2.0e-118:597:95//AC005754  
 F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:60//AC006037  
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//AF050079  
 F-NT2RP2000079//H.sapiens CpG island DNA genomic MseI fragment, clone 40c2, forward read cpg40c2.ft1k.//3.2e-33:197:95//Z55440  
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338  
 F-NT2RP2000091//HS\_2228\_A2\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363  
 F-NT2RP2000097  
 F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-05:482:60//AC004961  
 F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//AC003973  
 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356  
 F-NT2RP2000120//HS\_3000\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365  
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein m



RNA, complete cds.//4.2e-119:607:96//AF054177

F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827

F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419

F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSS and GSSs, complete sequence.//0.45:377:58//AL034370

F-NT2RP2000157//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC005924

F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431

F-NT2RP2000173

F-NT2RP2000175

F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//AL007295

F-NT2RP2000195//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSS and GSSs, complete sequence.//7.6e-62:170:99//AL023581

F-NT2RP2000205

F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete sequence.//7.2e-80:170:90//AC003030

F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//5.5e-64:400:85//AC004382

F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine B

ombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms,  
a predicted CpG island, ESTs and STSS.//2.2e-07:280:66//Z97632  
F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (M  
AG) mRNA, complete cds.//8.8e-30:508:67//U88401  
F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, comple  
te sequence.//4.0e-79:504:87//AC004066  
F-NT2RP2000248  
F-NT2RP2000257//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0078:286:60//AL021388  
F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 23  
49P21, genomic survey sequence.//5.7e-82:416:97//AQ059184  
F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323),  
complete sequence.//4.5e-29:310:73//AC006116  
F-NT2RP2000274  
F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//6  
.3e-20:260:73//X74904  
F-NT2RP2000288  
F-NT2RP2000289  
F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of  
HPF1, -2, and -9.//4.6e-69:744:70//M27877  
F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9.//4.4e-05:502:59//AL0  
21530  
F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.1e-13:173  
:76//AC006082  
F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome  
1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehyd  
rogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF  
6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains  
ESTs and GSSs, complete sequence.//8.3e-144:731:95//AL022398

F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12  
 Contains ESTs and GSSs, complete sequence.//1.9e-102:555:90//AL034430

F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//6.4e-105:639:87//M25757

F-NT2RP2000337//HS\_2060\_B1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2060 Col=1 Row=J, genomic survey sequence.//0.78:218:60//AQ243333

F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.6e-129:627:97//U83981

F-NT2RP2000369//HS\_2182\_B1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence.//2.5e-87:421:99//AQ024835

F-NT2RP2000412//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSS and GSSs.//0.72:170:65//AL021327

F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//5.0e-66:375:93//L28010

F-NT2RP2000420//Homo sapiens full length insert cDNA YQ86E07.//9.2e-77:423:93//AF075093

F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//2.1e-126:609:96//AF102265

F-NT2RP2000438//CITBI-E1-2519019.TR CITBI-E1 Homo sapiens genomic clone 2519019, genomic survey sequence.//0.96:61:78//AQ276878

F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.1e-17:341:67//AC004691

F-NT2RP2000459//H.sapiens mRNA for imogen 38.//5.7e-21:158:87//Z68747

F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//3.2e-11:160:73//Z92844

F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete

sequence.//0.0031:187:66//AC005229

F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence.//8.8e-07:179:64//AL026277

F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence.//0.19:72:81//U21671

F-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//5.0e-115:570:96//AL022318

F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds./8.4e-37:196:98//AB005543

F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.81:354:60//AC005321

F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//1.3e-149:732:97//AB014514

F-NT2RP2000644//HS\_3211\_A1\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=11 Row=K, genomic survey sequence.//3.6e-42:282:86//AQ175486

F-NT2RP2000656

F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386

F-NT2RP2000668

F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916

F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913

F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122

F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540

F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42  
unordered pieces.//0.97:115:70//AC004965

F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1  
(LIMK1) gene, complete cds.//9.7e-16:162:77//U62293

F-NT2RP2000764//HS\_2254\_B2\_D07\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey  
sequence.//0.071:45:95//AQ068887

F-NT2RP2000809

F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:6  
4//AF069698

F-NT2RP2000814

F-NT2RP2000816

F-NT2RP2000819

F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390  
:70//AB002292

F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.  
2e-44:255:93//Y09479

F-NT2RP2000845

F-NT2RP2000863//Human partial cDNA sequence, clone x874;.//5.9e-29:173:9  
4//Z47045

F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2  
.4e-140:732:94//AB018284

F-NT2RP2000892

F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//3  
.4e-129:610:98//AB018266

F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequ  
ence.//1.8e-37:212:84//AC005014

F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from t  
he tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Conta

ins ESTs and CpG island.//1.6e-126:682:93//Z69890  
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5  
 .8e-112:533:98//AB018298  
 F-NT2RP2000965  
 F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 2  
 2q12.1. Contains ESTs, STSS and GSSs and genomic marker D22S56, complete  
 sequence.//9.2e-101:505:96//AL021393  
 F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complet  
 e sequence.//1.6e-72:498:82//AC005277  
 F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete  
 sequence.//7.4e-12:171:77//AC002394  
 F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete s  
 equence.//1.2e-37:390:76//AC004167  
 F-NT2RP2001044//HS\_2253\_B1\_G01\_MF CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey s  
 equence.//0.21:276:61//AQ069224  
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
 0488.//3.2e-144:696:97//AB007957  
 F-NT2RP2001065  
 F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA,  
 complete cds.//4.3e-104:775:81//U91561  
 F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//  
 3.7e-69:488:82//AF000423  
 F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X conta  
 ins STS.//7.4e-11:490:61//Z86063  
 F-NT2RP2001119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596  
 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519  
 :63//D87072

F-NT2RP2001137//HS\_2193\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence.//1.8e-11:136:78//AQ032187

F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//6.2e-29:247:78//AC000076

F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LC B-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.23:207:66//AL009178

F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949

F-NT2RP2001174//RPCI11-58L2.TK RPCI11 Homo sapiens genomic clone R-58L2, genomic survey sequence.//7.6e-07:196:64//AQ237306

F-NT2RP2001196

F-NT2RP2001218

F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893

F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:68.1:72//X51760

F-NT2RP2001245//HS\_3062\_B1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177

F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353

F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430

F-NT2RP2001290//M.musculus mRNA for I47 clone.//8.6e-102:641:86//X61455  
 F-NT2RP2001295//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
 \* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594  
 F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//M  
 22967  
 F-NT2RP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//M  
 80783  
 F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 233  
 5A5, genomic survey sequence.//1.3e-65:366:94//AQ038539  
 F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070  
 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8  
 e-31:325:77//AJ003147  
 F-NT2RP2001366//H.sapiens CpG island DNA genomic MseI fragment, clone 4e  
 11, forward read cpg4e11.f1a.//1.7e-12:98:92//Z61305  
 F-NT2RP2001378//HS\_3054\_B2\_A03\_MR CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey s  
 equence.//9.8e-17:131:89//AQ100721  
 F-NT2RP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371  
 F-NT2RP2001392//S.pristinaespiralis snbC gene & snbDE gene.//0.019:267:5  
 9//Y11548  
 F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X conta  
 ins ESTs STS, CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z9  
 3242  
 F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-6  
 3:419:84//AF080219  
 F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//  
 3.1e-98:747:79//U76759  
 F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds.//3.7e-34:269:85//  
 AF015454



F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065

F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702

F-NT2RP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350

F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//X95275

F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931

F-NT2RP2001450

F-NT2RP2001467

F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence.//7.9e-14:151:80//AQ109561

F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2 C mRNA, complete cds.//2.6e-22:462:64//AF005355

F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL AR1.//2.0e-136:657:97//Y14494

F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-37:357:64//AC004596

F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//1.6e-103:384:94//AF035586

F-NT2RP2001560

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA 0488.//4.4e-123:590:98//AB007957

F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.038:580:58//U32943

F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds.//6.5e-09:222:66//AF030430

F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340

F-NT2RP2001613

F-NT2RP2001628//H.sapiens (xs128) mRNA, 380bp.//1.7e-15:279:68//Z36784

F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//5.4e-123:606:96//AF030233

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//4.2e-144:687:97//AF058718

F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enolase.//1.0e-36:372:74//X84907

F-NT2RP2001675//S.pombe chromosome I cosmid c2G11.//0.070:507:59//Z54354

F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//2.0e-60:232:96//AC005259

F-NT2RP2001678//HS\_2007\_A2\_A04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699

F-NT2RP2001699//RPCI11-57B17.TK RPCI11 Homo sapiens genomic clone R-57B17, genomic survey sequence.//0.99:141:63//AQ115592

F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//9.4e-117:604:95//AC004079

F-NT2RP2001721//Homo sapiens DNA sequence from clone 466I8 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//1.0:273:61//AL030998

F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR

Region, complete sequence.//1.0:356:62//AC000090

F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds.//3.7e-18:151:86//D14697

F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.0e-145:715:97//AC004783

F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:60//AE001378

F-NT2RP2001839//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347

F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610

F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219

F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309

F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.8e-87:496:92//AL031864

F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//9.2e-112:633:90//M74161

F-NT2RP2001900//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone R08A5, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281

F-NT2RP2001907//H.sapiens CpG island DNA genomic MseI fragment, clone 97f11, forward read cpg97f11.ft1a.//4.2e-26:206:84//Z64125

F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688

F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosm

id Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856

F-NT2RP2001943//Drosophila melanogaster cosmid 25E8.//0.00036:248:60//AL009196

F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.8e-8:232:99//AC005033

F-NT2RP2001947//Homo sapiens full length insert cDNA clone ZD81B04.//2.0e-28:172:94//AF086442

F-NT2RP2001969//H.sapiens CpG island DNA genomic MseI fragment, clone 152a8, reverse read cpg152a8.rtl1a.//1.0e-20:123:99//Z59378

F-NT2RP2001976

F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117

F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022

F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299

F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//0.76:189:65//AC005895

F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-12:160:79//AC004825

F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029

F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//2.2e-86:722:77//AC004552

F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375

F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//

9.7e-11:480:60//Z73301

F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//U87306

F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein {alternatively spliced, exon 10 to 13 region} [human, Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083

F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96//AF052183

F-NT2RP2002078//F12016-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//0.14:191:64//AQ249805

F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917

F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8e-111:533:97//AJ007509

F-NT2RP2002105//H.sapiens CpG island DNA genomic MseI fragment, clone 10h8, forward read cpg10h8.ft1a.//2.4e-29:178:94//Z58857

F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey sequence.//2.5e-32:202:92//B64468

F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//M25874

F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63//D85923

F-NT2RP2002172//HS\_3020\_B1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169

F-NT2RP2002185//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//2.8e-18:109:100//AQ201833

F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl) mRNA, complete cds.

//2.7e-36:363:78//U09215

F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein K  
ChAP mRNA, complete cds.//9.5e-82:477:89//AF032872

F-NT2RP2002208

F-NT2RP2002219//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL4P1, WORKING DRAFT SEQUENCE.//1.0:378:58//AL034557

F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic  
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC0  
05308

F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete c  
ds.//0.59:341:60//J03998

F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81  
:398:87//U22394

F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cd  
s.//6.6e-50:315:89//AF005418

F-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 118J21, WORKING DRAFT SEQUENCE.//9.7e-67:340:89//AL033527

F-NT2RP2002270//RPCI11-77C23.TV RPCI11 Homo sapiens genomic clone R-77C2  
3, genomic survey sequence.//2.9e-18:79:93//AQ268098

F-NT2RP2002292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 321D2, WORKING DRAFT SEQUENCE.//1.0:290:60//AL031033

F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA,  
partial cds.//1.5e-93:467:96//AF069532

F-NT2RP2002316//HS\_2171\_B2\_D11\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2171 Col=22 Row=H, genomic survey  
sequence.//7.3e-94:463:97//AQ119673

F-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//3.9e-123:64  
0:95//AB015594

F-NT2RP2002333

F-NT2RP2002373//F.rubripes GSS sequence, clone 026F10aB8, genomic survey  
sequence.//0.46:234:61//Z87330

F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant m  
RNA, complete cds.//9.4e-138:673:97//AF038958

F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A  
).//0.79:421:56//X95275

F-NT2RP2002408//F.rubripes GSS sequence, clone 080G11aA8, genomic survey  
sequence.//5.7e-15:220:71//AL015615

F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9.//7.1e-71:582:80//AJ22374  
2

F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3.//0.0018:210:67//AF0  
16682

F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1.//2.8e-18:295:67//U8  
8169

F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, comp  
lete sequence.//1.9e-06:281:66//AC004381

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.039:207:6  
3//D42045

F-NT2RP2002475

F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complet  
e cds.//2.4e-123:607:96//AB005289

F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//0.73:395:57//AF069300

F-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//7.2  
e-18:134:90//AC006213

F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1  
.2e-157:761:97//AB018334

F-NT2RP2002520

F-NT2RP2002537

F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRA

FT SEQUENCE, 7 unordered pieces.//0.83:252:60//AC004127  
F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing  
DNA polymerase gamma (polg) gene, complete sequence.//5.9e-93:186:99//AC  
005317  
F-NT2RP2002591//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304  
F-NT2RP2002595//Sequence 2 from patent US 5763220.//1.5e-84:430:95//AR01  
2155  
F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//1.9e-43:28  
2:87//U19181  
F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, parti  
al cds.//1.5e-11:99:90//AF051310  
F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice va  
riant, 1316 bp.//5.6e-27:460:63//Y10806  
F-NT2RP2002621  
F-NT2RP2002643//Rat calmodulin III gene for calmodulin; promoter region  
and exon 1.//0.023:322:60//D90397  
F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q2  
4.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384  
F-NT2RP2002701//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 50024, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380  
F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980  
F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2  
.5e-40:631:65//AB014572  
F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:6  
00:73//AF041107  
F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL03338  
8  
F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface prot



ein (PSSP15) gene, complete cds; ORF, 5' end.//0.0073:274:66//M94861  
 F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e-29:628:62//D89016  
 F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296  
 F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequence.//1.7e-08:206:63//AC002433  
 F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs.//2.8e-71:195:89//Z82171  
 F-NT2RP2002769//Streptomyces fradiae tylactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//0.0016:412:60//U78289  
 F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey sequence.//6.8e-18:186:79//B69837  
 F-NT2RP2002800  
 F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.2e-41:134:94//AC006078  
 F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone TRB-4.//0.85:93:68//M18845  
 F-NT2RP2002862//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=0, genomic survey sequence.//5.0e-67:390:91//AQ186344  
 F-NT2RP2002880  
 F-NT2RP2002891//CIT-HSP-2310014.TF CIT-HSP Homo sapiens genomic clone 2310014, genomic survey sequence.//0.11:53:90//AQ019792  
 F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511  
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//AF038392

F-NT2RP2002929//F.rubripes GSS sequence, clone 123I23aA1, genomic survey  
sequence.//3.9e-06:66:83//AL017246

F-NT2RP2002939

F-NT2RP2002954

F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, c  
omplete cds.//1.3e-47:411:79//U62483

F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP Homo sapiens genomic clone 23  
40D12, genomic survey sequence.//4.6e-96:476:97//AQ057233

F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A522  
30

F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete  
cds.//2.4e-09:272:61//AF059569

F-NT2RP2002987//Homo sapiens (subclone 6\_d9 from P1 H21) DNA sequence, c  
omplete sequence.//1.0e-22:293:67//AC000958

F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA,  
complete cds.//4.0e-74:502:84//AF025424

F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE,  
21 unordered pieces.//2.3e-46:474:76//AC004765

F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complet  
e sequence.//4.2e-23:202:82//AC005703

F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contai  
ns ESTs.//3.4e-59:330:82//Z83822

F-NT2RP2003099//HS\_3008\_B2\_C09\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey  
sequence.//1.4e-71:362:96//AQ089786

F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR0143  
62

F-NT2RP2003117//HS\_2034\_B2\_D12\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey

sequence.//1.5e-88:461:96//AQ230797

F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765

F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329

F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915

F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976

F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG:16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716

F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025

F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657

F-NT2RP2003164

F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43:334:79//U91328

F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040

F-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597

F-NT2RP2003206

F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794

F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:86//AF023657

F-NT2RP2003237//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447

F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107

F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//6.0e-114:696:87//L38481

F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833

F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525

F-NT2RP2003280//RPCI11-14I2.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-14I2, genomic survey sequence.//6.4e-77:400:95//B85286

F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024

F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973

F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//6.1e-85:416:97//AB006572

F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase.//0.60:309:64//X62722

F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666

F-NT2RP2003308//D.melanogaster crn mRNA.//1.1e-63:697:70//X58374

F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//0.040:145:64//AC005288

F-NT2RP2003339

F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence.//0.12:275:60//AL034559

F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510

F-NT2RP2003391

F-NT2RP2003393//HS\_3218\_A2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356

F-NT2RP2003394

F-NT2RP2003401

F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630

F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//2.1e-49:301:72//AP000023

F-NT2RP2003446

F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.0018:366:60//AJ235272

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//7.5e-16:189:68//AC004770

F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-25:197:85//M21977

F-NT2RP2003499

2.1e-08:408:61//AB000826

F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-33:192:96//AC005236

F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB11, partial cds.//1.0:328:60//AB013801

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-76:403:93//D87460

F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:151:95//X03702

F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.3e-101:564:91//M21977

F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6.//2  
.0e-40:315:75//Z80899

F-NT2RP2003543

F-NT2RP2003559//H.sapiens CpG island DNA genomic MseI fragment, clone 90  
a5, reverse read cpg90a5.rtl1a.//1.1e-20:122:99//Z56144

F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.  
//8.8e-27:664:63//M34551

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds.//4.  
1e-113:541:98//AB007931

F-NT2RP2003581

F-NT2RP2003596//F.rubripes GSS sequence, clone 036L10aF12, genomic surve  
y sequence.//1.9e-11:210:65//AL012756

F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA,  
complete cds.//1.9e-123:587:98//AF030233

F-NT2RP2003629

F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthe  
tase.//7.8e-88:582:84//AJ006215

F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18  
unordered pieces.//5.6e-47:335:83//AC005081

F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human B  
AC library) complete sequence.//1.2e-06:133:74//AC003684

F-NT2RP2003691//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 525L6, WORKING DRAFT SEQUENCE.//1.7e-47:337:81//AL023807

F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complet  
e cds.//1.3e-65:458:82//U44803

F-NT2RP2003704//H.sapiens CpG island DNA genomic MseI fragment, clone 2a  
9, reverse read cpg2a9.rtl1e.//3.8e-17:170:84//Z60615

F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.  
6e-108:518:98//AB011097

F-NT2RP2003713//HS\_2016\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=9 Row=D, genomic survey sequence.//1.3e-11:102:90//AQ226895

F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.4e-27:249:78//AC003973

F-NT2RP2003727//RPCI11-77I19.TV RPCI11 Homo sapiens genomic clone R-77I19, genomic survey sequence.//3.4e-26:294:74//AQ268303

F-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.6e-74:194:91//AC004951

F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence.//1.7e-92:165:96//AC003964

F-NT2RP2003760//B.primigenius mRNA for coat protein gamma-cop.//4.5e-76:696:73//X92987

F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence.//1.0:109:69//AB013275

F-NT2RP2003769

F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//3.0e-96:467:98//AC004771

F-NT2RP2003777

F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//7.2e-107:731:82//S70011

F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey sequence.//7.0e-20:124:95//AQ038761

F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//8.9e-06:151:74//AC004491

F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.//0.018:145:69//AC005167

F-NT2RP2003857//HS\_3227\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=M, genomic survey s

equence.//0.96:257:61//AQ303467

F-NT2RP2003859

F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.0e-12:369:65//AC002375

F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey sequence.//0.13:167:64//AQ265722

F-NT2RP2003912//nek1=serine/threonine- and tyrosine-specific protein kinase [mice, erythroleukemia cells, mRNA, 4263 nt].//1.3e-136:838:86//S45828

F-NT2RP2003952

F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//AB014458

F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloprotease in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein in S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL031282

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347

F-NT2RP2003984

F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENC



E, 11 unordered pieces.//1.7e-26:260:77//AC000382  
F-NT2RP2003988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681  
F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 C  
ontains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:9  
1//AL023580  
F-NT2RP2004014  
F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequ  
ence.//5.8e-83:427:87//AC004780  
F-NT2RP2004042  
F-NT2RP2004066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 134019, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555  
F-NT2RP2004081  
F-NT2RP2004098//HS\_2216\_A1\_B12\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey  
sequence.//1.0e-07:86:84//AQ145694  
F-NT2RP2004124//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey s  
equence.//3.0e-25:155:94//AQ136993  
F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon  
e: K8K14, complete sequence.//1.0:220:62//AB007645  
F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)),  
complete sequence.//0.93:480:56//AC002493  
F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 geno  
mic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61  
//AC005140  
F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, c  
omplete cds.//1.0:162:66//AF028235  
F-NT2RP2004172//S.pombe chromosome II cosmid c24E9.//1.7e-06:466:59//AL0

21816

F-NT2RP2004187//Homo sapiens full length insert cDNA YQ86E07.//3.5e-17:3  
54:64//AF075093

F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//  
9.4e-53:397:82//AF003998

F-NT2RP2004196

F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to  
exons 23 through 34.//0.0023:386:61//M60676

F-NT2RP2004226//HS\_2186\_A1\_D03\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, genomic survey s  
equence.//7.8e-58:370:87//AQ063813

F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34:448:67/  
/X75756

F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds./  
/5.2e-108:510:99//AB015718

F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 n  
t. position (6/7).//1.1e-12:489:61//AP000006

F-NT2RP2004242

F-NT2RP2004245

F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:62//AL0  
34446

F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequ  
ence.//3.5e-11:299:64//AC005781

F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete c  
ds.//4.5e-150:735:97//AF000416

F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110 (D147))  
, complete sequence.//0.98:267:59//AC004423

F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete  
sequence.//1.6e-40:419:75//AC002519

F-NT2RP2004347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650

F-NT2RP2004364

F-NT2RP2004365

F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427:57//AL031864

F-NT2RP2004373//Homo sapiens cosmids Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397

F-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969

F-NT2RP2004392

F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164

F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467:64//AJ004799

F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441

F-NT2RP2004412//H.sapiens CpG island DNA genomic MseI fragment, clone 34g4, reverse read cpg34g4.rt1a.//5.0e-27:154:98//Z65369

F-NT2RP2004425

F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9.//0.0053:196:65//AL021530

F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377:63//AL034388

F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591

F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-0

7:815:57//AL034556

F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890

F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163

F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85:484:91//AQ239555

F-NT2RP2004568//H.vulgare GAA-satellite DNA.//2.0e-07:292:62//Z50100

F-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755

F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908

F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020

F-NT2RP2004600

F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109:73//AC005176

F-NT2RP2004614

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496:98//AJ006291

F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:98//AB007929

F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:239:61//AC005805

F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3. Contains an EST and GSSs, complete sequence.//1.0:236:61//AL031312

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:94//AB014525

F-NT2RP2004709//HS\_2033\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187:74//AQ230714

F-NT2RP2004710//HS\_3185\_B2\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110:84//AQ172885

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:96//AB007947

F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138:71//Z78022

F-NT2RP2004767//H.sapiens CpG island DNA genomic MseI fragment, clone 65c11, reverse read cpg65c11.rt1a.//1.3e-24:217:81//Z62210

F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//1.6e-45:541:71//AF024636

F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697:59//AE001398

F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-53:353:84//U56252

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953

F-NT2RP2004802

F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495:97//AF054179

F-NT2RP2004841//Human DNA sequence from cosmid J138017, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//7.6e-82:531:84//Z72519

F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040017bA3, genomic survey sequence.//0.96:183:64//AL025645

F-NT2RP2004897//Human Chromosome X clone bW XD187, complete sequence.//4.

8e-142:710:96//AC004383

F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82  
:418:95//AB007144

F-NT2RP2004936

F-NT2RP2004959//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Lib  
ry D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey  
sequence.//3.5e-25:218:83//AQ150183

F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1  
(KS1) mRNA, complete cds.//2.5e-59:339:79//U56732

F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-lik  
e protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, an  
d sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-19:187:7  
2//U91328

F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020  
:297:61//Z98551

F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.2  
2:162:69//L29029

F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4,  
genomic survey sequence.//0.13:273:61//B12642

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431  
:65//D63478

F-NT2RP2004999

F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:  
240:63//X63375

F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6  
.0e-159:782:97//AB014515

F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200

F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:  
501:96//AF100141

F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//AC004849

F-NT2RP2005020

F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-43:98:93//AC000380

F-NT2RP2005031//HS\_2052\_B2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464

F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454

F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//0.20:519:57//AC005696

F-NT2RP2005108

F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564

F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//X98743

F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//0.00024:547:59//AJ223012

F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//0.95:191:62//AC004527

F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583

F-NT2RP2005147//HS\_3184\_A1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226

F-NT2RP2005159//H.sapiens CpG island DNA genomic MseI fragment, clone 132g6, forward read cpg132g6.ft1a.//1.1e-13:93:97//Z59162

F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U1

3070

F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125:633:96//AJ007509

F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:60//U80808

F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//AC005189

F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536

F-NT2RP2005254

F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R).//0.58:132:65//X87513

F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666

F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26335

F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//AF060219

F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590

F-NT2RP2005293//HS\_3245\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454

F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576

F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166:90//U11701

F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//0.39:353:62//AF032387



F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138

F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//Z92844

F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:96//AF072247

F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358

F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184

F-NT2RP2005407

F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:62//AC005346

F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//4.0e-107:532:97//AQ055548

F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//1.0:239:61//B97865

F-NT2RP2005457//B.taurus CI-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647

F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679

F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//6.5e-18:152:75//AC006116

F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36 .11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo)gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2, TBPII, TNF-R2, CD120B, TNFBR). Contains ESTs,

STSSs, GSSs, genomic marker D1S434 and a ca repeat polymorphism, complete sequence.//4.4e-12:89:97//AL031276

F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463:73//AC004130

F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.2e-115:228:99//AC006030

F-NT2RP2005491//HS\_2253\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=M, genomic survey sequence.//4.6e-23:234:80//AQ116847

F-NT2RP2005495

F-NT2RP2005496//HS\_3064\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097

F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931

F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10 q25, complete sequence.//0.86:183:63//AC005880

F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U82695

F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:444:92//AF092563

F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307

F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282:60//M14993

F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449

F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963

F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:89//AF046734

F-NT2RP2005555//HS\_2188\_A2\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195:65//AQ086723

F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//2.5e-44:473:71//AF062529

F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//0.99:213:65//AC005016

F-NT2RP2005600//H.sapiens CpG island DNA genomic MseI fragment, clone 172d12, reverse read cpg172d12.rt1a.//0.32:134:63//Z57359

F-NT2RP2005605

F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//9.8e-91:447:97//AF062085

F-NT2RP2005622

F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556

F-NT2RP2005637//NATI (NATI\*10)=acetyltransferase 1 {3' region, polyadenylation polymorphism} [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:65//S78829

F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980

F-NT2RP2005645//HS\_2201\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763

F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493

F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626

F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605

F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//AF089814

F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405

F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836

F-NT2RP2005694

F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPCI11-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183

F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342

F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III.//0.86:117:64//X89603

F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367

F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//AC002528

F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627

F-NT2RP2005732//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017

F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270

F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342

F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF068868

F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516

F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853

F-NT2RP2005767//G.gallus PB1 gene.//2.1e-73:544:80//X90849

F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836

F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//D11336

F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds.//0.96:184:60//AB015853

F-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423

F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//AF010579

F-NT2RP2005812

F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103

F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086

F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873

F-NT2RP2005853//RPCI11-24D4.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490

F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:829:98//AF092564

F-NT2RP2005859//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553

F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103I24aF4, genomic sur

vey sequence.//7.8e-06:92:79//AL027276  
F-NT2RP2005886//HS\_3187\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885  
F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-32:660:66//L11316  
F-NT2RP2005901//H.sapiens CpG island DNA genomic MseI fragment, clone 15b5, reverse read cpg15b5.rtl1a.//0.0026:66:84//Z54729  
F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.4e-49:481:75//AC004241  
F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840  
F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770  
F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//1.0e-48:533:71//AC005207  
F-NT2RP2006023//HS\_3048\_A1\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553  
F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence.//3.9e-06:102:74//B51912  
F-NT2RP2006043//Human intercrine-alpha (HIRH) mRNA, complete cds.//1.9e-05:418:59//U19495  
F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//AF016861  
F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047  
F-NT2RP2006071  
F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete

sequence.//0.46:264:59//AF027207

F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//  
AC004073

F-NT2RP2006103//HS\_2254\_A2\_D02\_MR CIT Approved Human Genomic Sperm Lib  
ry D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey s  
equence.//5.7e-27:156:96//AQ129602

F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1  
.2e-62:655:71//AC000378

F-NT2RP2006141//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 537K23, WORKING DRAFT SEQUENCE.//1.2e-69:316:98//AL034405

F-NT2RP2006166//Homo sapiens chromosome 4 clone B32I8, complete sequence  
./3.1e-45:387:81//AC004063

F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransfer  
ase Lec4A cell line point mutant mRNA, complete cds.//0.99:111:73//U6258  
7

F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.  
8e-113:567:96//AB014554

F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-2  
8:718:62//AC005232

F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKIN  
G DRAFT SEQUENCE, 66 unordered pieces.//6.5e-83:239:94//AC006057

F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X964  
84

F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 230  
OP9, genomic survey sequence.//2.0e-18:118:97//AQ012480

F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein ra8 mRNA,  
complete cds.//7.6e-102:635:86//U49055

F-NT2RP2006258//RPCI11-9N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11  
-9N9, genomic survey sequence.//8.6e-05:181:63//B71615

F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK./  
/0.44:111:71//X97630

F-NT2RP2006275//Pseudorabies virus UL [5,6,7,8,8.5,9,10,11,12,13] genes./  
/2.0e-05:501:59//X97257

F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138  
:679:97//AF035262

F-NT2RP2006320//P.falciparum pfmdrl gene.//0.00013:425:60//X56851.

F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete  
sequence.//4.1e-19:545:62//AC003973

F-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 745I14, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532

F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, comp  
lete sequence.//6.2e-125:602:98//AC004893

F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequ  
ence.//2.1e-06:241:65//AC005514

F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic sur  
vey sequence.//7.8e-06:148:70//AL029590

F-NT2RP2006393//Human DNA sequence from clone 80I19 on chromosome 6p21.3  
1-22.2 Contains genes and pseudogenes for olfactory receptor-like protei  
ns, STS, GSS, complete sequence.//6.8e-06:167:70//AL022727

F-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone Y313F4, WORKING DRAFT SEQUENCE.//4.2e-92:363:84//AL023808

F-NT2RP2006441

F-NT2RP2006454//Sequence 8 from Patent W09517522.//2.9e-06:180:66//A4533  
8

F-NT2RP2006456

F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545:98//A  
J006266

F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons



encoding chl-ch4 and secretion domains, partial cds.//0.061:201:66//U50149

F-NT2RP2006472

F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSS, GSSs and a CA repeat polymorphism, complete sequence.//8.8e-10:273:66//Z93929

F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6.//0.71:174:59//U40965

F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//6.6e-114:669:90//AF038966

F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1.//6.0e-26:503:63//M20855

F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome.//0.44:134:71//U60315

F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140:85//U50537

F-NT2RP3000002//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-32:214:89//U14571

F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637:98//AJ011972

F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:571:60//L14320

F-NT2RP3000047

F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.0e-67:626:74//M27877

F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394:64//AC001227

F-NT2RP3000068

F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//1.0:301:61//AC004746

F-NT2RP3000080//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//1.9e-44:297:79//AL021391

F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528:65//U12536

F-NT2RP3000092//RPCI11-22M5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22M5, genomic survey sequence.//3.3e-27:157:97//B84237

F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds.//0.92:185:64//L29260

F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.2e-112:286:89//AC005189

F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//9.0e-181:849:98//AB011164

F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//4.2e-24:155:94//AC005884

F-NT2RP3000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//7.2e-43:269:81//AL023583

F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9.//0.098:405:57//L39063

F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence.//0.96:608:55//AC004716

F-NT2RP3000220

F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.0e-18:509:58//AF059569

F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence.//3.5e-05:224:65//AC004101

F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds.//2.1e-109:691:86//D86972

F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence./  
/0.20:119:68//Z70213  
F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence.//9.8e-78:174  
:88//AF065393  
F-NT2RP3000255  
F-NT2RP3000267  
F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, comp  
lete cds.//5.9e-48:374:82//U48853  
F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds.//4.  
9e-22:583:63//J02932  
F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-1  
1-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107  
F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, co  
mplete cds.//5.5e-26:283:79//U78090  
F-NT2RP3000333//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533  
F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome X  
p11.3-11.4. Contains STSS and the DXS7 locus with GT and GTG repeat poly  
morphisms, complete sequence.//6.7e-42:465:74//Z97181  
F-NT2RP3000348  
F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence.//3.4e-79:174  
:88//AF065393  
F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, co  
mplete cds.//2.2e-127:816:85//M25757  
F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing fact  
or, complete cds.//0.0075:288:58//D83743  
F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete  
cds.//7.1e-134:693:94//L04966  
F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:30

8:60//AJ011318

F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//  
0.00012:441:58//Z72642

F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cd  
s.//5.0e-174:841:97//AF071185

F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053\_B\_8, comple  
te sequence.//7.9e-53:817:68//AC006083

F-NT2RP3000433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681

F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic su  
rvey sequence.//4.0e-19:169:81//AL026471

F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contai  
ns ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG isla  
nd.//2.4e-41:459:65//Z84488

F-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650

F-NT2RP3000451//HS\_2024\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2024 Col=19 Row=I, genomic survey  
sequence.//0.011:367:57//AQ229420

F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 233  
8P5, genomic survey sequence.//1.5e-89:458:96//AQ055548

F-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353

F-NT2RP3000487//H.sapiens CpG island DNA genomic MseI fragment, clone 11  
b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z64440

F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X  
16667

F-NT2RP3000526//Homo sapiens full length insert cDNA clone YZ38E04.//4.1  
e-30:283:76//AF086071

F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966

F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260

F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554

F-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//9.0e-171:827:98//AC006012

F-NT2RP3000562

F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597

F-NT2RP3000584

F-NT2RP3000590//H.sapiens CpG island DNA genomic MseI fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723

F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868

F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305

F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043

F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320

F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128

F-NT2RP3000622//HS\_3213\_A2\_D02\_T7.CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104

F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890

F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313

F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363

F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.2e-46:421:77//AC005089

F-NT2RP3000661

F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237

F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961

F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872

F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930

F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264

F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-37:429:70//U16655

F-NT2RP3000753

F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence  
./2.8e-38:519:69//Z99281

F-NT2RP3000815//HS\_2237\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence./0.79:151:61//AQ067252

F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds./0.36:378:58//L39387

F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds./0.0025:291:62//U02513

F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4./0.69:563:57//M29009

F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments./2.1e-46:666:68//Z86062

F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence./3.4e-92:193:93//AC005581

F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02./3.4e-32:261:81//D16938

F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces./5.1e-44:358:81//AC005082

F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast. plant and worm proteins. Contains

ns ESTs and STSS, complete sequence.//4.4e-123:150:98//AL021940  
 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831  
 F-NT2RP3000865  
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445  
 F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367  
 F-NT2RP3000875//HS\_2236\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence.//0.98:153:68//AQ154007  
 F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds.//0.44:213:65//AF021340  
 F-NT2RP3000904//Rat Na<sup>+</sup> channel mRNA, 3' end.//3.6e-106:505:99//M27223  
 F-NT2RP3000917//Mouse mRNA for Dhml protein, complete cds.//3.1e-132:691:93//D38517  
 F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//3.2e-97:585:88//AF015264  
 F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:89//U91326  
 F-NT2RP3000980//R.norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335  
 F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529  
 F-NT2RP3001004//H.sapiens CpG island DNA genomic MseI fragment, clone 39c1, reverse read cpg39c1.rt1a.//5.9e-27:150:99//Z60925  
 F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:610:57//AC006039  
 F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7



; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23  
:352:67//AC005653

F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:43  
7:77//X78927

F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, com  
plete cds.//8.4e-50:534:74//AF060219

F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.  
2e-14:474:60//AB018325

F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 230  
5P8, genomic survey sequence.//3.4e-37:222:93//AQ021278

F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712  
:64//D86969

F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing  
DNA polymerase gamma (polg) gene, complete sequence.//2.7e-116:186:99//A  
C005317

F-NT2RP3001111

F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers D  
XS366 and DXS87 on chromosome X.//2.4e-05:702:58//Z68871

F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete  
sequence.//1.9e-170:821:98//AC005189

F-NT2RP3001116//HS\_3075\_A1\_F01\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3075 Col=1 Row=K, genomic survey s  
equence.//7.3e-49:290:92//AQ120581

F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-  
25.3 Contains exon from gene similar to 40S ribosomal protein, first cod  
ing exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequ  
ence.//1.4e-121:598:97//AL031864

F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U0936

F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39  
, UL40 and UL41.//6.8e-05:344:64//Z49078

F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA  
, partial cds.//0.00021:529:60//AF027735

F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.  
6e-179:851:98//AB018305

F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-1  
1-3M16, genomic survey sequence.//2.1e-15:106:96//B48859

F-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 423B22, WORKING DRAFT SEQUENCE.//2.0e-159:418:95//AL034379

F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//A  
J006266

F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.  
1-41 Contains GSS, complete sequence.//1.1e-69:207:97//AL034351

F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 geno  
mic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//  
AC005507

F-NT2RP3001216//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//3.3e-05:561:56//AC004845

F-NT2RP3001221

F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-1  
1:120:87//D12619

F-NT2RP3001236

F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protei  
n.//3.9e-19:501:61//X51396

F-NT2RP3001245//CITBI-E1-2505C1.TF.1 CITBI-E1 Homo sapiens genomic clone  
2505C1, genomic survey sequence.//8.5e-70:337:100//AQ242007

F-NT2RP3001253//CITBI-E1-2505N14.TR CITBI-E1 Homo sapiens genomic clone  
2505N14, genomic survey sequence.//0.83:235:60//AQ260430

F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3  
.8e-47:761:64//AB018269

F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and  
partial cds.//2.3e-64:618:72//AF027513

F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosi  
ne-phosphorylated protein.//2.6e-99:669:83//Y18101

F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M860  
4 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561

F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complet  
e sequence.//5.9e-39:304:70//AC005837

F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544  
:69//D87457

F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.  
4e-27:547:63//AF047465

F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomi  
c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60/  
/AC004709

F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF07  
8790

F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345  
:73//D86966

F-NT2RP3001339//Rattus norvegicus mytonic dystrophy kinase-related Cdc42  
-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935

F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//  
5.3e-27:247:81//AF083105

F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Re  
gion, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000  
052

F-NT2RP3001356

F-NT2RP3001374

F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628

F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332

F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-pter. Contains STS, complete sequence.//0.045:359:61//Z82198

F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296

F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046

F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//5.4e-20:245:73//AC005521

F-NT2RP3001407//RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031

F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327

F-NT2RP3001426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447

F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997

F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//8.5e-73:431:91//U69668

F-NT2RP3001432//HS\_3032\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619

F-NT2RP3001447

F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.2

1-36.33. Contains the alternatively spliced gene for Matrix Metalloprotease in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031282

F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065

F-NT2RP3001457

F-NT2RP3001459

F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//AF072836

F-NT2RP3001490

F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395

F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//8.5e-171:804:98//AF064801

F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete cds.//8.9e-140:743:91//U36499

F-NT2RP3001529//Streptomyces griseus DNA for ribosomal protein L21, ribosomal protein L27, Obg, complete cds.//2.1e-14:517:59//D87916

F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic

survey sequence.//4.7e-05:217:63//AF078176

F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds.//4.3e-17:332:67//M83196

F-NT2RP3001580//RPCI11-91E19.TV RPCI11 Homo sapiens genomic clone R-91E19, genomic survey sequence.//4.2e-15:110:91//AQ281332

F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104

F-NT2RP3001589//RPCI11-68M15.TK RPCI11 Homo sapiens genomic clone R-68M15, genomic survey sequence.//8.7e-108:517:98//AQ237629

F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//1.0e-09:257:65//AC004674

F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane monooxygenase A beta chain and methane monooxygenase component C genes, complete cds.//0.59:450:57//M90050

F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.8e-42:278:79//AL021808

F-NT2RP3001629

F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978

F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.018:127:66//Z68117

F-NT2RP3001646

F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449

F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-38:542:66//U49793

F-NT2RP3001676//HS\_3090\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250

F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3 ; P1 clone DS01859, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539 :57//AC004358

F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11. //2.8e-130:355:96//AB020860

F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//2.1e-37:512:70//AF059273

F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 230 0P9, genomic survey sequence.//2.8e-19:123:95//AQ012480

F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9.4e-11:167:74//D319 62

F-NT2RP3001708//H.sapiens CpG island DNA genomic MseI fragment, clone 4g 7, reverse read cpg4g7.rt1d.//1.3e-17:113:97//Z61312

F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein.//2.2e-95:601:88//X 99642

F-NT2RP3001716

F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.4e-159:565:97//AF054177

F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//1.7e-132:786:88//AF008554

F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds.//3.9e-104:811 :78//D50918

F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGC R Region, complete sequence.//6.5e-07:178:69//AC000097

F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11. 3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat

, STS, complete sequence.//5.2e-31:311:77//AL031311

F-NT2RP3001753//Sequence 29 from patent US 5658882.//0.11:513:58//I62381

F-NT2RP3001764//Sequence 6 from Patent W09706245.//6.4e-47:673:66//A5988

8

F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10.//0.078:290:63//U39

644

F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//2.

8e-151:710:98//AB007928

F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA,

partial cds.//1.2e-26:213:85//U13262

F-NT2RP3001799//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 469D22, WORKING DRAFT SEQUENCE.//8.4e-51:168:95//AL031284

F-NT2RP3001819//S.glaucescens genes strU, strX, strV and strW for 5'-hyd

roxystreptomycin prduction and transport polypeptides.//0.084:526:58//X

89010

F-NT2RP3001844//HS\_3110\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey

sequence.//1.5e-40:232:82//AQ140433

F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic

sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.14:452:58//ACO

05505

F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknox1) mRNA, comp

lete cds.//2.7e-39:575:67//AF061270

F-NT2RP3001857//M.musculus tex292 mRNA (5' region).//8.7e-07:106:81//X804

34

F-NT2RP3001896

F-NT2RP3001898//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 163G9, WORKING DRAFT SEQUENCE.//0.094:456:60//AL008733

F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence./



/0.58:482:56//Z73969

F-NT2RP3001926//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*

from MAL4P1, WORKING DRAFT SEQUENCE.//0.42:401:58//AL034557

F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//3.1e-28:263:77//AC004651

F-NT2RP3001931

F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence.//3.6e-24:182:91//B95475

F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//1.8e-165:815:96//AB014575

F-NT2RP3001944

F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844

F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), 01 (o1), 03 (o3), 02 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//8.2e-10:564:60//AF030694

F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//2.5e-57:361:80//Z83822

F-NT2RP3002004//Sequence 3 from patent US 5798245.//1.6e-26:104:100//ARO25386

F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137

F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//1.3e-32:334:68//AC004640

F-NT2RP3002033//H.sapiens DNA sequence.//0.012:214:63//Z22493

F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773

F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.6e-12:613:60//AL021841

F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249

F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682

F-NT2RP3002062

F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.24:508:58//AJ235272

F-NT2RP3002081//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//9.7e-22:155:90//AQ218494

F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//9.6e-66:562:77//AC006210

F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence.//5.9e-16:214:74//AQ018040

F-NT2RP3002108

F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020

F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds.//0.96:434:60//AF003370

F-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING DRAFT SEQUENCE.//1.3e-63:380:91//AL031710

F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742

F-NT2RP3002163

F-NT2RP3002165//M.musculus HCNGP mRNA.//1.4e-142:867:87//X68061

F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete

sequence.//0.090:394:59//AC006121

F-NT2RP3002173//HS\_3062\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence.//3.3e-101:509:96//AQ193219

F-NT2RP3002181//Human DNA sequence from clone 24018 on chromosome 6p21.3 1-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//4.5e-106:432:84//AL021808

F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.63:353:60//AC005321

F-NT2RP3002248//HS\_3029\_A1\_D10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence.//3.5e-10:125:79//AQ094880

F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end.//5.6e-09:629:59//L14321

F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//4.9e-35:366:74//B03004

F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex.//0.023:326:60//X64898

F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.//3.8e-12:643:57//AE000810

F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-09:490:60//AC005504

F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches.//1.9e-93:572:88//Z49862

F-NT2RP3002343//HS\_3010\_A2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence.//9.0e-75:373:97//AQ119068

F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.9e-64:588:75//X16396

F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form.//1.3e-164:770:98//Y16355

F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds.//1.4e-190:911:98//AB018331

F-NT2RP3002399

F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//7.2e-25:249:79//D89340

F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//1.2e-138:649:99//AB014578

F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence.//5.0e-18:115:96//B78927

F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence.//0.00020:170:65//Z49068

F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence.//1.6e-59:308:97//AF091088

F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds.//1.4e-144:763:93//U35246

F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.8e-178:833:98//AB018272

F-NT2RP3002549//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-26:123:72//AC004821

F-NT2RP3002566//Streptomyces viridifaciens sigma factor (hrdD) gene, complete cds.//0.76:459:59//U60418

F-NT2RP3002587//Homo sapiens chromosome Y, clone 264,M,20, complete sequ

ence.//4.6e-13:199:76//AC004617  
 F-NT2RP3002590//*Porphyra purpurea* chloroplast, complete genome.//0.88:28  
 4:60//U38804  
 F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK *Homo sapiens* genomic cl  
 one A-441H11, genomic survey sequence.//2.0e-22:140:95//B68331  
 F-NT2RP3002603  
 F-NT2RP3002628//*C.acetobutylicum* dnaJ and orfB genes.//2.0e-05:333:60//X  
 69050  
 F-NT2RP3002631  
 F-NT2RP3002650//*Mus musculus* mRNA for cartilage-associated protein (CASP  
 ).//1.5e-20:641:62//AJ006469  
 F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes.//5.2e-05:621:59  
 //Z78205  
 F-NT2RP3002660//*Homo sapiens* PAC clone DJ1006K12 from 7q31.2-q31, comple  
 te sequence.//0.98:453:57//AC004946  
 F-NT2RP3002663//*Homo sapiens* chromosome 19, cosmid F6697, complete seque  
 nce.//3.3e-22:407:67//AC006129  
 F-NT2RP3002671//*S.pombe* chromosome III cosmid c553.//1.0e-12:336:66//AL0  
 23704  
 F-NT2RP3002682//*Caenorhabditis elegans* cosmid F17C11, complete sequence.  
 //1.3e-21:448:64//Z72507  
 F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK *Homo sapiens* genomic clone  
 A-789B1, genomic survey sequence.//2.5e-25:173:91//B51656  
 F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cd  
 s.//1.2e-73:728:74//D17577  
 F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 *Homo sapiens* genomic clone  
 2507L14, genomic survey sequence.//0.0012:55:92//AQ263530  
 F-NT2RP3002713  
 F-NT2RP3002763//*Caenorhabditis elegans* cosmid T20F10, complete sequence.

//0.98:209:63//Z81594

F-NT2RP3002770

F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds.//0.78:515:57//AF029325

F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//1.9e-21:167:79//AL022718

F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//0.32:187:66//AC005549

F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715

F-NT2RP3002861//Caenorhabditis elegans cosmid M03F4.//4.2e-05:226:65//U64601

F-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.0e-93:638:83//AF030430

F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:88//AB001895

F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//7.9e-12:160:78//AC006087

F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314

F-NT2RP3002911//RPCI11-24N15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24N15, genomic survey sequence.//2.3e-13:442:61//B88815

F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500

F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:793:98//AC005754

F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024

F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666

F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820

F-NT2RP3002978//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505

F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.92:341:60//AC001644

F-NT2RP3002988//HS\_3015\_A1\_B07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708

F-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:197:79//AF109905

F-NT2RP3003032//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-80, complete sequence.//1.6e-08:809:58//AL010153

F-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//4.1e-111:804:81//U78090

F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1).//1.4e-12:633:59//X16609

F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//0.034:282:60//AC002410

F-NT2RP3003071//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12.rtlc.//6.8e-15:95:100//Z64565

F-NT2RP3003078

F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, co

mplete cds.//8.1e-72:732:71//D88315

F-NT2RP3003121

F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.5e-12:168:76//AC004510

F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//4.0e-148:908:87//D12646

F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//U17995

F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639

F-NT2RP3003150

F-NT2RP3003157//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489

F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete cds.//8.6e-06:228:65//AF064868

F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933

F-NT2RP3003197

F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//4.1e-48:640:67//AF015264

F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:81//U31059

F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799

F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//6.3e-75:776:74//U20286

F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:74//AJ006064

F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.



//3.7e-128:617:98//AF055460

F-NT2RP3003251//H.sapiens Staf50 mRNA.//3.5e-67:651:76//X82200

F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153

F-NT2RP3003278//H.sapiens CpG island DNA genomic.MseI fragment, clone 28 b4, forward read cpg28b4.ft1a.//4.0e-27:174:93//Z60555

F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131:694:93//L36983

F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds.//1.7e-64:662:71//AF004162

F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//D85610

F-NT2RP3003302//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.6e-95:680:82//AC006213

F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//1.0:191:62//AC004527

F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7.//0.0084:403:61//AL031107

F-NT2RP3003327//H.sapiens Staf50 mRNA.//2.5e-29:253:67//X82200

F-NT2RP3003330

F-NT2RP3003344

F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//9.0e-41:296:84//AC005284

F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).//0.047:404:60//AL021069

F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//8.3e-122:632:96//AC005519

F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT

SEQUENCE, 17 unordered pieces.//0.0036:127:74//AC000360  
 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//2.0e-110:843:79//  
 U09874  
 F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//  
 AC002407  
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA,  
 complete cds.//1.0e-20:430:63//U90653  
 F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, comp  
 lete cds.//4.2e-139:524:90//AF071317  
 F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C  
 Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequ  
 ence.//8.8e-18:111:97//B40173  
 F-NT2RP3003433//HS\_2219\_B2\_A11\_MF CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey  
 sequence.//1.2e-57:410:83//AQ145866  
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete c  
 ds.//5.2e-181:853:98//AF004828  
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.  
 6e-173:826:98//AB018268  
 F-NT2RP3003491//CIT-HSP-234401.TR CIT-HSP Homo sapiens genomic clone 234  
 401, genomic survey sequence.//1.2e-39:213:97//AQ057124  
 F-NT2RP3003500//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey  
 sequence.//0.025:253:60//AQ090347  
 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL),  
 complete sequence.//0.95:279:60//AC004234  
 F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequ  
 ence.//1.8e-88:166:84//AC006049  
 F-NT2RP3003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985  
 F-NT2RP3003564//HS\_3141\_B1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798  
 F-NT2RP3003572  
 F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632  
 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387  
 F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:463:84//AC004235  
 F-NT2RP3003625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600  
 F-NT2RP3003656  
 F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271  
 F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096  
 F-NT2RP3003672  
 F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811  
 F-NT2RP3003686//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993  
 F-NT2RP3003701  
 F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-107:788:82//U42975  
 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2

.3e-148:700:98//AB018300

F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785

F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGRIB, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326

F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458

F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031

F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321

F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801

F-NT2RP3003819

F-NT2RP3003825

F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543:62//X17626

F-NT2RP3003831//RPCI11-50N15.TJ RPCI11 Homo sapiens genomic clone R-50N15, genomic survey sequence.//1.1e-21:174:85//AQ082633

F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242:98//AF070611

F-NT2RP3003842//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143:97//AQ195884

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335:68//AB018268

F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805:99//AB018343

F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709:84//U19181

F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.//8.9e-11:193:70//U20554

F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//2.6e-47:404:77//AF057358

F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC005504

F-NT2RP3003989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661

F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds.//0.021:433:58//U58837

F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//1.4e-164:838:94//X84692

F-NT2RP3004016//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726

F-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400

F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774:67//AB002317

F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSS and GSSs, complete sequence.

//7.9e-17:484:62//AL021939

F-NT2RP3004078//M.musculus (BALB/c) MRFX2 mRNA.//1.9e-102:684:83//X76089

F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17  
, genomic survey sequence.//0.021:207:63//B09433

F-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//3.5e-25:272:77//AC005038

F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete  
sequence.//8.6e-28:223:73//AC003973

F-NT2RP3004125//Homo sapiens TTF-I interacting peptide 20 mRNA, partial  
cds.//2.2e-28:637:63//AF000560

F-NT2RP3004145

F-NT2RP3004148

F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6  
.5e-120:578:98//AF032900

F-NT2RP3004189//M.musculus tex292 mRNA (5' region).//1.1e-06:102:82//X804  
34

F-NT2RP3004206//D.melanogaster crn mRNA.//7.3e-69:715:71//X58374

F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 pre  
cursor, complete cds.//4.8e-42:650:66//D64009

F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequen  
ce.//8.4e-55:184:84//D42052

F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), c  
omplete sequence.//0.22:458:60//AC006084

F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence./  
/1.6e-29:409:69//Z22181

F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q  
25, complete sequence.//3.6e-117:242:100//AC005385

F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//  
X69353

F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-88:489:91//AF013967

F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733:98//AF088982

F-NT2RP3004282//Homo sapiens torsina (DYT1) mRNA, complete cds.//1.3e-24:597:61//AF007871

F-NT2RP3004332

F-NT2RP3004334//L.esculentum gene for fruit ripening polygalacturonase./0.23:501:57//X80908

F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020

F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877

F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025

F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7 ; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653

F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249

F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678

F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206

F-NT2RP3004451//RPCI11-51J15.TK RPCI11 Homo sapiens genomic clone R-51J15, genomic survey sequence.//8.8e-19:180:82//AQ052326

F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917

F-NT2RP3004466//HS\_3038\_B2\_F08\_MF CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458

F-NT2RP3004470//H.sapiens CpG island DNA genomic MseI fragment, clone 81 all, reverse read cpg81a11.rtl1a.//7.0e-25:148:96//Z56029

F-NT2RP3004472//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//1.6e-20:143:92//AQ052792

F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925

F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//U47024

F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851

F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//4.0e-67:265:84//AC006023

F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.2e-55:415:78//AC004673

F-NT2RP3004504//M.musculus mRNA for CPEB protein.//2.0e-110:618:91//Y08260

F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//AC005328

F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574

F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316

F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532

F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126

F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emzf1)



mRNA, complete cds.//6.9e-18:433:64//AF031955  
 F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2  
 522H6, genomic survey sequence.//5.3e-15:138:84//AQ280780  
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRN  
 A, complete cds.//1.0e-179:860:97//AF026445  
 F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4  
 .2e-150:711:98//AB007946 .  
 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//A  
 J006266  
 F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1  
 unordered pieces.//9.3e-14:360:65//AC004977  
 F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2  
 C mRNA, complete cds.//2.9e-52:539:73//AF005355  
 F-NT2RP3004669//Brn-3a=class V POU transcription factor [mice, CD/CD, em  
 bryo fibroblast cells, Genomic, 2160 nt].//0.046:437:57//S69350  
 F-NT2RP3004670//Human DNA sequence \*\*\*. SEQUENCING IN PROGRESS \*\*\* from c  
 lone 356B8, WORKING DRAFT SEQUENCE.//1.9e-05:625:59//Z98882  
 F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete  
 sequence.//1.5e-155:844:92//AC006121  
 F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon  
 e: K24G6, complete sequence.//0.012:417:59//AB012242  
 F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequen  
 ce.//8.0e-18:242:74//AC005035  
 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-  
 81:556:85//AF029761  
 F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP  
 ).//1.6e-19:654:63//AJ006469  
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5  
 e-149:720:97//AJ012449

F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:36:57//AL034558

F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538

F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931

F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952

F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776

F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681

F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088

F-NT2RP4000159//RPCI11-75N16.TJ RPCI11 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551

F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210

F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989

F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600

F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300

F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.8e-161:751:99//AC005261

F-NT2RP4000218//RPCI11-69B7.TJ RPCI11 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504

F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470

F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA,  
complete cds.//2.1e-120:707:87//U72523

F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence./  
/2.8e-128:604:99//AF091092

F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 23  
36N24, genomic survey sequence.//0.27:124:69//AQ043515

F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//  
8.6e-32:619:63//Z71408

F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:  
63//D63481

F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene,  
complete cds.//6.9e-05:756:59//U59322

F-NT2RP4000323

F-NT2RP4000355

F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2  
.0e-140:654:99//AB018281

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (   
IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195

F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome;  
segment 3/4.//2.0e-23:524:62//AJ235272

F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//I30  
536

F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, co  
mplete cds, strain:BALB/c.//4.3e-05:450:58//D63850

F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323),  
complete sequence.//9.2e-37:336:69//AC006116

F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U5696

6

F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:

69//AL021086

F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.6e-42:265:81//AC003101

F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194

F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183

F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982

F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499

F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483

F-NT2RP4000481

F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125

F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904

F-NT2RP4000515

F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//1.6e-179:851:98//AC006238

F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203:93//AJ010840

F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk 2/tyro3) gene, alternative 5' coding exon 2C.//0.26:162:61//U23720

F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498

F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386

F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)),  
complete sequence.//1.3e-05:498:58//AC002443

F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//I054  
65

F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, c  
loned into cosmid vector pEMBLcos2, complete sequence.//2.5e-53:183:82//  
AF059580

F-NT2RP4000588//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 414D7, WORKING DRAFT SEQUENCE.//0.00062:253:65//AL033543

F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complet  
e cds.//3.2e-138:666:98//AF067730

F-NT2RP4000638//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey  
sequence.//3.0e-06:78:89//AQ099333

F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA bi  
nding protein and Myc-associated zinc finger protein, complete cds.//1.9  
e-11:104:85//AB017335

F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene,  
exon 1.//0.34:350:62//AF100904

F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone  
IMAGE:300856.//3.3e-167:785:99//AB004852

F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cd  
s.//3.7e-07:261:65//U61149

F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//  
X82272

F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.  
1e-41:350:71//AB011178

F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, c  
omplete cds.//1.0:504:58//L19301

F-NT2RP4000739//CIT-HSP-2010022.TR CIT-HSP Homo sapiens genomic clone 2010022, genomic survey sequence.//1.1e-24:161:93//B57903

F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917

F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//9.6e-18:259:68//U22818

F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939

F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//AC005189

F-NT2RP4000837//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//2.1e-128:644:97//AL034420

F-NT2RP4000839//RPCI11-6D8.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6D8, genomic survey sequence.//1.5e-44:281:91//B48216

F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515

F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367

F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//AJ001616

F-NT2RP4000879//N.tabaccum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804

F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//D45913

F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901

F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-08:609:58//AC004290

F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:87//U42975

F-NT2RP4000927//H.sapiens genomic DNA (chromosome 3; clone NRL062R).//0.75:175:62//X87547

F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//AF069532

F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC004688

F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.0e-128:673:96//AC005519

F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657

F-NT2RP4000975//CIT-HSP-2307I6.TF CIT-HSP Homo sapiens genomic clone 2307I6, genomic survey sequence.//6.5e-31:317:79//AQ015742

F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942

F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823

F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911

F-NT2RP4000996//Panaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358

F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424

F-NT2RP4001004

F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176

F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140

F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086

F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170

F-NT2RP4001057

F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469

F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124

F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018

F-NT2RP4001080//H.sapiens PTB-4 gene for polypirimidine tract binding protein.//9.0e-64:628:70//X65372

F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164

F-NT2RP4001095

F-NT2RP4001100//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402

F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:87//M96629

F-NT2RP4001122

F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668

F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969

F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079

F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095

F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, c



complete cds.//3.0e-48:581:66//D67067

F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952

F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476

F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494

F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rsc 19) mRNA, partial cds.//0.032:453:58//U82511

F-NT2RP4001207//HS\_2248\_A1\_C03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358

F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019018 map 10 p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877

F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251

F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657

F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059569

F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081

F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds.//1.0:459:59//U33061

F-NT2RP4001260//Sequence 2 from Patent W09601901.//0.0018:246:63//A48324

F-NT2RP4001274//Homo sapiens, complete sequence.//2.5e-05:201:67//AC005854

F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence.//3.5e-18:138:92//AQ040728

F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40

) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.4e-30:535:65//AF043250

F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//3.5e-145:795:91//AJ001119

F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870

F-NT2RP4001339//HS\_3205\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence.//7.1e-24:305:73//AQ183725

F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence.//1.9e-17:106:91//AC004918

F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase.//7.6e-40:631:66//X91011

F-NT2RP4001351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//2.7e-30:608:64//AL031428

F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7.//0.23:540:57//AL031107

F-NT2RP4001372//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//8.5e-23:129:100//AQ051701

F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1.//0.15:213:61//X78609

F-NT2RP4001375

F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311\_F\_12, complete sequence.//7.3e-28:153:88//AC005722

F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.2e-47:518:73//AC004691

F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.00079:686:57//J03998

F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds.//2.0e-76:818:

71//D86957

F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein.//3.5e-87:839:73//X78933

F-NT2RP4001442

F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds.//0.21:218:63//AB018326

F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884

F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds.//2.5e-59:480:75//D10523

F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//9.7e-39:392:72//AF049612

F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat.//2.7e-24:147:96//X61693

F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds.//0.87:583:58//M32513

F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.93:394:58//AC005308

F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.1e-143:820:89//U20086

F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w.//2.2e-05:319:61//Z71663

F-NT2RP4001551//S.pombe chromosome II pl p8B7.//0.64:335:60//AL032684

F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.0:309:58//AC004806

F-NT2RP4001567//HS\_2166\_B1\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey

sequence.//0.99:188:59//AQ086290

F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds.//7.0e-53:566  
:72//D79989

F-NT2RP4001571//RPCI11-21F20.TP RPCI-11 Homo sapiens genomic clone RPCI-  
11-21F20, genomic survey sequence.//2.8e-19:119:97//B85885

F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop.//5.8e-129  
:813:85//X92987

F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//3.4e-131:795:8  
6//AJ223830

F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase.//1.3e-14:66  
3:59//X74219

F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9  
(Lawrence Livermore human cosmid library) complete sequence.//6.4e-10:  
135:73//AC002364

F-NT2RP4001614//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey  
sequence.//3.4e-06:78:89//AQ099333

F-NT2RP4001634

F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cos  
mid Homo sapiens genomic clone cSRL-161F1, genomic survey sequence.//4.9  
e-12:144:76//B02870

F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.  
//3.8e-69:437:86//Y11092

F-NT2RP4001656//HS\_2013\_A1\_D01\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2013 Col=1 Row=G, genomic survey s  
equence.//2.0e-30:207:89//AQ224793

F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.23:105:7  
1//L49362

F-NT2RP4001679//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 462023, WORKING DRAFT SEQUENCE.//2.7e-45:351:84//AL031431  
F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.8e-30:163:88//U96629  
F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.1e-13:402:63//AC004296  
F-NT2RP4001730//RPCI11-37M21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-37M21, genomic survey sequence.//0.88:177:67//AQ029840  
F-NT2RP4001739  
F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTELO0023.seq.//4.9e-36:192:98//Z96232  
F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:86//L11316  
F-NT2RP4001790//Homo sapiens clone NH0569I24, complete sequence.//1.4e-29:327:74//AC005678  
F-NT2RP4001803  
F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-16:576:60//AF054841  
F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAPI2 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence.//2.1e-08:601:59//Z98743  
F-NT2RP4001828  
F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-53:555:73//D31888  
F-NT2RP4001841  
F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572  
F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691  
F-NT2RP4001889//HS\_2052\_B1\_H06\_T7 CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425

F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//AC005014

F-NT2RP4001896//T3B4TFC TAMU Arabidopsis thaliana genomic clone T3B4, genomic survey sequence.//0.99:354:61//B26193

F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.//0.031:409:60//AB011413

F-NT2RP4001927//HS\_2216\_B1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677

F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046

F-NT2RP4001946//HS\_3021\_B2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185

F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSSs and GSSs, complete sequence.//2.1e-18:421:65//AL022577

F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey sequence.//0.030:358:61//AQ005028

F-NT2RP4001966//Mus musculus DOC4 (Doc4) mRNA, complete cds.//2.5e-68:812:68//AF059485

F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.9e-57:555:75//AC003976

F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//8.9

e-21:123:98//B01950

F-NT2RP4002047//*Saccharomyces cerevisiae* chromosome XII cosmid 8003.//1.

6e-29:520:64//U17243

F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP *Homo sapiens* genomic clone 2045A15, genomic survey sequence.//2.8e-22:137:96//B80243

F-NT2RP4002058//T20L11-T7 *Arabidopsis thaliana* genomic clone T20L11, genomic survey sequence.//0.019:141:65//AQ248640

F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP *Homo sapiens* genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223

F-NT2RP4002075//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841

F-NT2RP4002078//RPCI11-73M20.TJ RPCI11 *Homo sapiens* genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030

F-NT2RP4002081//*F.rubripes* GSS sequence, clone 190022bB9, genomic survey sequence.//0.0024:350:60//Z92062

F-NT2RP4002083//*M.musculus* tex27 mRNA.//8.2e-77:456:89//X80437

F-NT2RP4002408//*Caenorhabditis elegans* serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515

F-NT2RP4002791

F-NT2RP4002888//*Homo sapiens* BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383

F-NT2RP4002905//*Homo sapiens* chromosome 17, clone hRPC.842\_A\_23, complete sequence.//6.5e-91:672:83//AC004662

F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197

F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901

F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380

F-NT2RP5003492

F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-11  
1:623:93//Z81365

F-NT2RP5003506//H.sapiens CpG island DNA genomic MseI fragment, clone 71h2, reverse read cpg71h2.rtl1a.//1.4e-49:283:93//Z62703

F-NT2RP5003512//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312

F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236

F-NT2RP5003524//Homo sapiens beta-spectrin (HSpTB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178

F-NT2RP5003534//H.sapiens CpG island DNA genomic MseI fragment, clone 14c10, forward read cpg14c10.ft1b.//0.00013:70:91//Z54631

F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934

F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510

F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933

F-OVARC1000013

F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922

F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674

F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:238:89//AF064603

F-OVARC1000058



F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625

F-OVARC1000068//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883

F-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387

F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259

F-OVARC1000087//HS\_2004\_B2\_E11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037

F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489

F-OVARC1000092//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.1e-10:720:58//AC004617

F-OVARC1000106//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369

F-OVARC1000109

F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250

F-OVARC1000114//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574

F-OVARC1000133//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027

F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640

F-OVARC1000145//HS\_2257\_B2\_D11\_MR CIT Approved Human Genomic Sperma Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854

F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703

F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I64695

F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764

F-OVARC1000191//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557

F-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604

F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332

F-OVARC1000212//F.rubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910

F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//I81226

F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194

F-OVARC1000288

2.2e-22:181:83//J00345

F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-192A9, genomic survey sequence.//4.8e-18:110:99//B18003

F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574

F-OVARC1000309

F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12

unordered pieces.//3.1e-122:325:95//AC005236  
 F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1  
 C) mRNA, complete cds.//4.0e-46:339:84//U19614  
 F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF0  
 36696  
 F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:25  
 2:59//AC005007  
 F-OVARC1000384//Homo sapiens expanded SCA7 CAG repeat.//2.2e-09:276:64//  
 AF020275  
 F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing K  
 vLQT1 gene, complete sequence.//0.61:343:59//AC003693  
 F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0  
 .075:242:60//Z28201  
 F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete seq  
 uence.//0.00088:285:62//AC005166  
 F-OVARC1000420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718  
 F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete  
 sequence.//4.9e-30:195:84//AC005826  
 F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-0  
 5:651:59//AL034558  
 F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M741  
 65  
 F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99/  
 /U09284  
 F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12  
 .2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR  
 (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3), and another member of the  
 Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678

F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1  
 .0e-138:566:99//AB014583

F-OVARC1000461

F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1  
 ) mRNA, complete cds.//4.7e-124:650:93//AF023451

F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, comp  
 lete sequence.//1.0e-15:510:59//AC004221

F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic  
 survey sequence.//2.5e-06:272:62//AJ227191

F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed o  
 f complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829

F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome  
 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronection,  
 Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S rib  
 osomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, g  
 enomic marker D1S2691 and STSs.//1.7e-13:709:60//Z99297

F-OVARC1000496//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031733

F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.1e-113:5  
 39:99//AF051850

F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17  
 unordered pieces.//8.0e-149:716:98//AC005024

F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequ  
 ence.//5.8e-137:545:97//AC004510

F-OVARC1000543//HS\_3055\_A2\_F10\_MF CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey  
 sequence.//0.19:104:71//AQ102820

F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome  
 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS.

CpG island, complete sequence.//4.4e-136:670:97//AL022069  
 F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//1.3e-15:262:69//AC002985  
 F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733  
 F-OVARC1000573//HS\_3241\_B1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942  
 F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.7e-97:445:90//AC002414  
 F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//9.1e-27:354:72//AC003973  
 F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//0.97:276:62//AL023775  
 F-OVARC1000605  
 F-OVARC1000622//Homo sapiens (subclone 2\_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648  
 F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772  
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162  
 F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244  
 F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7./

/1.6e-81:291:84//AJ001713

F-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424

F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds  
./1.5e-151:549:99//AF027156

F-OVARC1000689//nbxb0003aG01f CUGI Rice BAC Library Oryza sativa genomic  
clone nbxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003

F-OVARC1000700

F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene  
, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925

F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltra  
nsferase mRNA, complete cds.//3.7e-109:451:91//AF038661

F-OVARC1000730

F-OVARC1000746

F-OVARC1000769//HS\_2056\_B2\_G06\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic survey  
sequence.//8.8e-19:147:86//AQ245905

F-OVARC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78  
//X95403

F-OVARC1000781//Sequence 5 from Patent W09722695.//1.9e-89:705:78//A6355  
2

F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, compl  
ete sequence.//3.0e-131:631:98//AC004542

F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete seq  
uence.//1.7e-32:295:80//AC003691

F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUEN  
CE, 99 unordered pieces.//3.2e-55:356:88//AC004469

F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9  
.5e-27:163:94//Y17711

F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543

F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584

F-OVARC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963

F-OVARC1000876//S.cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125

F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086

F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to kata).//0.25:231:61//Z82044

F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721

F-OVARC1000890

F-OVARC1000891

F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494

F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcript on control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320

F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172

F-OVARC1000924//HS\_2022\_A1\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493

F-OVARC1000936//Human PAC clone DJ0093I03 from Xq23, complete sequence.//1.2e-113:476:91//AC003983

F-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848

F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549

F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276

F-OVARC1000959//CIT-HSP-2348016.TR CIT-HSP Homo sapiens genomic clone 2348016, genomic survey sequence.//0.99:270:59//AQ062850

F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat,./3.9e-41:577:72//AL009181

F-OVARC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270

F-OVARC1000971//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841

F-OVARC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274

F-OVARC1000996//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858

F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785

F-OVARC1001000//HS\_2247\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=0, genomic survey sequence.//3.1e-60:315:96//AQ153910

F-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//3.1e-124:595:98//AC004190

F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290

F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021



F-OVARC1001032//Yeast (*S.cerevisiae*) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451

F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533

F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149

F-OVARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-29:277:76//AC005081

F-OVARC1001044//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//0.0017:387:61//AL031319

F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein in CBP90 mRNA, partial cds.//0.012:112:74//AF053768

F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//I30292

F-OVARC1001062//nbxb0026H08r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026H08r, genomic survey sequence.//0.018:344:59//AQ271878

F-OVARC1001065//S.pombe chromosome I cosmid c29E6.//0.86:338:59//Z66525

F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082657

F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:65//AF003529

F-OVARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652:59//AL022153

F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333

F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897

F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86/

/AF015913

F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//6  
.4e-150:710:98//AF051782

F-OVARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53), co  
mplete sequence.//0.99:148:67//AC005178

F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENC  
E, 11 unordered pieces.//2.6e-35:302:74//AC000382

F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sapiens genomic clone 647  
P20, genomic survey sequence.//0.94:106:66//B79052

F-OVARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79  
//X62322

F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map 4q25, complet  
e sequence.//2.9e-90:496:84//AC004069

F-OVARC1001162

F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2  
unordered pieces.//0.00090:219:64//AC004961

F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the complete  
genome.//1.0:265:59//AE001141

F-OVARC1001170//H.sapiens (xs170) mRNA, 350bp.//4.6e-58:355:90//Z36823

F-OVARC1001171//CIT-HSP-2285E22.TF CIT-HSP Homo sapiens genomic clone 22  
85E22, genomic survey sequence.//1.5e-25:152:83//AQ002315

F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.  
1. Contains ESTs, STSS and GSSs, complete sequence.//0.0024:94:80//AL022  
323

F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gen  
e, complete cds.//1.0:356:60//AF063001

F-OVARC1001180//G.gallus DNA for polyubiquitin gene Ub II.//0.0062:275:6  
0//X58195

F-OVARC1001188//Homo sapiens full length insert cDNA clone ZD93F03.//1.8

e-32:180:97//AF086486  
 F-OVARC1001200  
 F-OVARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence./  
 /0.013:128:67//Z48334  
 F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENC  
 E, 44 unordered pieces.//3.7e-131:811:87//AC001235  
 F-OVARC1001243//Human BAC clone GS117010 from 7q21-q22, complete sequenc  
 e.//0.044:457:59//AC003078  
 F-OVARC1001244//Human homolog of Drosophila female sterile homeotic mRNA  
 , complete cds.//8.4e-18:118:95//M80613  
 F-OVARC1001261//Mus musculus putative membrane-associated guanylate kina  
 se 1 (Magi-1) mRNA, alternatively spliced c form, partial cds.//1.4e-95:  
 649:84//AF027505  
 F-OVARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPas  
 e activating protein mRNA, complete cds.//0.00051:72:83//U35776  
 F-OVARC1001270  
 F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.  
 1e-142:644:96//AB014543  
 F-OVARC1001282//RPCI11-60K8.TK RPCI11 Homo sapiens genomic clone R-60K8,  
 genomic survey sequence.//0.0089:285:58//AQ195857  
 F-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein h  
 omolog HuEMAP mRNA, complete cds.//3.0e-20:263:73//U97018  
 F-OVARC1001306//nbxb0002M13r CUGI Rice BAC Library Oryza sativa genomic  
 clone nbxb0002M13r, genomic survey sequence.//0.98:170:66//AQ156061  
 F-OVARC1001329//Homo sapiens BAC clone RG370M10 from 7p15, complete sequ  
 ence.//1.3e-05:432:61//AC003986  
 F-OVARC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomi  
 c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//A  
 C005504

F-OVARC1001339//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//0.76:89:74//AC006071

F-OVARC1001341//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402

F-OVARC1001342

F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=4 Row=0, genomic survey sequence.//1.5e-07:254:67//B44456

F-OVARC1001357//Homo sapiens Xp22-149 BAC RPCI11-46604 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC005297

F-OVARC1001360

F-OVARC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811

F-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801

F-OVARC1001376//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680

F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819

F-OVARC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287

F-OVARC1001399//CIT-HSP-2291I8.TR CIT-HSP Homo sapiens genomic clone 2291I8, genomic survey sequence.//1.7e-11:104:87//AQ007611

F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651

F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426

F-OVARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudogene similar to ribosomal protein S3A and part of

a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z99714

F-OVARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387

F-OVARC1001442//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.0:167:64//AL031687

F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS.//4.4e-64:376:79//Z84482

F-OVARC1001476//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone Y24F12, WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277

F-OVARC1001480

F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140

F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507

F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 complete genomic sequence, complete sequence.//1.2e-98:503:83//AC002039

F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411

F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//0.43:190:68//X69219

F-OVARC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.017:533:56//AC005140

F-OVARC1001555//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.4e-159:416:99//AC005037

F-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retroseu

dogene.//2.4e-115:540:99//AF031165  
F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//AF043945  
F-OVARC1001610//, complete sequence.//1.4e-12:152:77//AC005409  
F-OVARC1001611  
F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12  
Contains STS, GSS, complete sequence.//0.022:146:70//AL031682  
F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds./  
/6.5e-109:358:96//AB005543  
F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8  
e-47:393:81//AB006867  
F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 216  
4L6, genomic survey sequence.//0.94:85:69//B92840  
F-OVARC1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 317C6, WORKING DRAFT SEQUENCE.//1.9e-06:489:61//Z97651  
F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds.//1.0:  
262:59//U41662  
F-OVARC1001726//Human telomere associated repeat sequence, complete sequ  
ence.//7.5e-08:283:65//M57752  
F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606:81/  
/X12650  
F-OVARC1001745//HS\_3007\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey  
sequence.//0.00020:269:60//AQ164522  
F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL0  
23781  
F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eI  
F3, p35 subunit mRNA, complete cds.//4.2e-149:706:98//U97670  
F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3

.0e-115:580:96//AB014575

F-OVARC1001768

F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//5.7e-64:477:78//AC005066

F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:76//AC004704

F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence.//0.98:214:61//AQ264481

F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of a minoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//9.5e-151:712:99//AL023694

F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.7e-56:522:75//AF068748

F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete sequence.//1.7e-63:526:81//AC003662

F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS.//0.17:214:65//Z70224

F-OVARC1001820//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 445N2, WORKING DRAFT SEQUENCE.//3.2e-55:379:82//AL031779

F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//2.8e-17:509:62//AC005609

F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X.//0.35:403:58//Z73361

F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence.//2.4e-25:148:96//B94622

F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e-18:122:95//AF070611

F-OVARC1001879//HS\_3026\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence.//4.9e-29:204:87//AQ207748

F-OVARC1001880//Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds.//3.5e-05:489:60//U51127

F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-29:350:74//AC005020

F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//8.6e-56:300:96//AF061749

F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.3e-10:253:66//AL031904

F-OVARC1001911//HS\_2196\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069

F-OVARC1001916//HS\_3054\_B1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979

F-OVARC1001928

F-OVARC1001942//H.sapiens CpG island DNA genomic MseI fragment, clone 21d7, forward read cpg21d7.ft1a.//7.2e-12:83:98//Z60390

F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds.//3.5e-50:535:69//AF059179

F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds.//1.7e-16:294:67//U37263

F-OVARC1001950//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.5e-20:261:68//AJ011929

F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4.//0.99:447:57//Z1902

1

F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20



unordered pieces.//2.9e-19:178:83//AC005995  
 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence.//0.17:2  
 32:62//AL034559  
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//2.  
 1e-158:739:98//AB007934  
 F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr  
 ome region), segment 4/15, WORKING DRAFT SEQUENCE.//3.0e-17:781:59//AP00  
 0011  
 F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6  
 unordered pieces.//5.4e-136:683:96//AC006015  
 F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complet  
 e sequence.//1.0:220:61//AC004668  
 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//6.  
 1e-115:557:98//AF041483  
 F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete  
 sequence.//0.013:461:57//AC006241  
 F-OVARC1002138//Caenorhabditis elegans cosmid F32D1.//1.0e-29:545:64//AF  
 016427  
 F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 23  
 43H20, genomic survey sequence.//2.3e-11:258:67//AQ055576  
 F-OVARC1002156  
 F-OVARC1002158//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, g  
 enomic survey sequence.//1.8e-16:383:66//B11616  
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase.//0  
 .0041:300:64//X79568  
 F-OVARC1002182//F.rubripes GSS sequence, clone 123I23aA7, genomic survey  
 sequence.//1.4e-10:240:66//AL017241  
 F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 22  
 94H13, genomic survey sequence.//8.2e-10:158:75//AQ003859

F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:93//M12585

F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//3.8e-51:550:72//AF022789

F-PLACE1000014

F-PLACE1000031//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.91:333:61//AC004821

F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome X p22.11-Xp22.22. Contains ESTs STS and CpG island.//2.6e-20:279:67//Z93023

F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.6e-63:488:82//AC005177

F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508

F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-30:190:94//L22154

F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74//AC005521

F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.2e-09:143:73//AC005848

F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence.//0.52:390:60//AC002389

F-PLACE1000094

F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 C contains EST, STS, GSS and CpG Island, complete sequence.//4.4e-129:731:92//AL023580

F-PLACE1000142//H.sapiens AUH mRNA.//6.4e-09:328:62//X79888

F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//AF058291

F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//I7  
6211

F-PLACE1000213

F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic  
sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57/  
/AC005504

F-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 695020, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818

F-PLACE1000246//HS\_2008\_A2\_D04\_T7 CIT Approved Human Genomic Sperm Lib  
rary D Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey s  
equence.//0.96:153:61//AQ269813

F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T regio  
n.//5.1e-12:571:60//U11584

F-PLACE1000308//D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, t  
RNA-Gln & tRNA-Val.//0.00013:369:59//X54011

F-PLACE1000332//HS\_2016\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Lib  
rary D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey  
sequence.//7.5e-83:424:96//AQ232106

F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 23  
26A16, genomic survey sequence.//0.13:46:100//AQ047350

F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA  
, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//  
U19891

F-PLACE1000380//F.rubripes GSS sequence, clone 047P21aA10, genomic surve  
y sequence.//0.43:198:62//Z88163

F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA  
, partial cds.//8.7e-149:740:96//U58032

F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds  
.//0.22:484:56//D86074

F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867

F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.6e-85:421:87//AC005899

F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515

F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189

F-PLACE1000435//HS\_3217\_A2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698

F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-61:616:71//AC004382

F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580

F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete sequence.//1.1e-33:349:76//AC002491

F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//1.1e-34:256:83//U35245

F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276

F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484

F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409

F-PLACE1000564

F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//3.3e-46:631:68//M27877

F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA,

complete cds.//7.3e-84:503:88//M55542

F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449

F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276

F-PLACE1000610//HS\_2056\_A1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967

F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//AF044201

F-PLACE1000636

F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:96//AF102265

F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLC110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896

F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//8.0e-60:675:70//S78219

F-PLACE1000712

F-PLACE1000716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:266:82//B43026

F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8, genomic survey sequence.//0.023:157:68//AQ113109

F-PLACE1000749//Plasmodium falciparum MAL3P7, complete sequence.//0.099:664:57//AL034559

F-PLACE1000755//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00068:206:62//X76589

F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapiens genomic clone RPCI-

11-3J18, genomic survey sequence.//6.5e-08:93:89//B63806  
F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:98//AB014548  
F-PLACE1000786//Drosophila melanogaster cosmid 80H7.//1.4e-43:589:68//AL031027  
F-PLACE1000793//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12.rtlc.//4.6e-09:71:100//Z64565  
F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//5.0e-14:235:72//AC002310  
F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.013:404:60//AC006158  
F-PLACE1000849//H.sapiens CpG island DNA genomic MseI fragment, clone 72a10, reverse read cpg72a10.rtlc.//3.3e-09:82:92//Z62712  
F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935  
F-PLACE1000863//H.sapiens CpG island DNA genomic MseI fragment, clone 53d2, forward read cpg53d2.ft1b.//7.3e-37:199:98//Z55621  
F-PLACE1000909//H.sapiens CpG island DNA genomic MseI fragment, clone 173f8, reverse read cpg173f8.rtlc.//1.5e-17:128:92//Z57391  
F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//8.1e-55:647:72//AL009181  
F-PLACE1000948  
F-PLACE1000972//RPCI11-61B1.TJ RPCI11 Homo sapiens genomic clone R-61B1, genomic survey sequence.//1.0e-26:148:99//AQ194348  
F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572  
F-PLACE1000979//H.sapiens CpG island DNA genomic MseI fragment, clone 76e8, reverse read cpg76e8.rtlc.//2.7e-10:84:94//Z55963

F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8  
.0e-140:694:96//AB018267

F-PLACE1001000//Herpetomonas muscarum muscarum kinetoplast 12S rRNA gene  
./0.0056:443:58//U01011

F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 20  
13L15, genomic survey sequence.//0.99:277:58//B58681

F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:  
88//AC000357

F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete seq  
uence.//7.2e-33:333:73//AC004741

F-PLACE1001024

F-PLACE1001036//CIT-HSP-2373I10.TF CIT-HSP Homo sapiens genomic clone 23  
73I10, genomic survey sequence.//1.1e-80:393:98//AQ108662

F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon  
e: K9I9, complete sequence.//8.8e-40:483:66//AB013390

F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate reductas  
e/saccharopine dehydrogenase.//1.2e-23:224:80//AJ224761

F-PLACE1001076//HS\_2195\_B1\_D05\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2195 Col=9 Row=H, genomic survey s  
equence.//0.0014:168:66//AQ066659

F-PLACE1001088

F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-9  
5:489:96//AF065485

F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprote  
in (env) gene, partial cds.//0.0073:253:62//U81400

F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRN  
A, complete cds.//2.5e-64:676:71//AF022158

F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(  
6,12).//3.8e-26:174:93//M30702

F-PLACE1001168

F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-23:245:68//AC005603

F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSSs, GSSs and a putative CpG island, complete sequence.//0.010:102:70//AL031177

F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//9.3e-82:684:77//D14336

F-PLACE1001241

F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219

F-PLACE1001272//H.sapiens subunit of coatomer complex.//0.31:50:96//X70476

F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005507

F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320

F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642

F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X17617

F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:491:73//AC005282

F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey seq



uence.//9.6e-26:142:100//B31181

F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.

6e-25:155:95//AB018342

F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614

F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.

21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene,

EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324

F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08

:117:84//AJ001319

F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I573

40

F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes f

or beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11

:620:60//X52177

F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING

DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence./

/2.0e-69:365:96//AF091087

F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete

sequence.//8.2e-121:608:97//AC006241

F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENC

E, 8 unordered pieces.//1.3e-06:437:61//AC000384

F-PLACE1001456//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC lib

rary), complete sequence.//0.98:348:60//AC003106

F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome X

q22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148

F-PLACE1001484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660  
 F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene,  
 exon 1.//0.00015:333:59//L78720  
 F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)),  
 complete sequence.//0.00016:161:66//AC004373  
 F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-  
 21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs  
 .//3.7e-22:260:76//AL021786  
 F-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667  
 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete  
 sequence.//2.7e-139:482:96//AC005669  
 F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete seq  
 uence.//6.9e-116:681:89//AC005261  
 F-PLACE1001570//HS\_3105\_A1\_F06\_MR CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey  
 sequence.//1.2e-10:137:79//AQ139817  
 F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of  
 hepatocellular colorectal and non-small cell lung cancer , segment 3/11.  
 //1.8e-102:217:99//AB020860  
 F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternativ  
 ely spliced product, complete cds.//3.7e-104:501:98//AF069984  
 F-PLACE1001608//HS\_2189\_A1\_G07\_MR CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey  
 sequence.//2.9e-60:429:84//AQ221959  
 F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7  
 unordered pieces.//4.4e-114:552:98//AC005037  
 F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12  
 .3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene

similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587

F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341

F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032

F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//7.7e-159:788:97//AC005971

F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSS and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL022165

F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.1e-149:760:96//AC005921

F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200

F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958\_E\_11, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883

F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776

F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGL C Region, complete sequence.//1.0:274:59//AC000051

F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124

F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607

F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221

F-PLACE1001745

F-PLACE1001746//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744

F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243

F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842

F-PLACE1001761//HS\_3027\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972

F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394

F-PLACE1001781

1.3e-08:238:65//AC005637

F-PLACE1001799//HS\_3075\_B1\_H03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474

F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone : MRC8, complete sequence.//0.00035:196:66//AB020749

F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953

F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286

F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177

F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850

F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244

F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408

F-PLACE1001912

F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935

F-PLACE1001928//HS\_2220\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361

F-PLACE1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596

F-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755

F-PLACE1002004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996

F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337

F-PLACE1002052//HS\_2178\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908

F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284

F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178

F-PLACE1002090//Homo sapiens full length insert cDNA clone ZA85C09.//7.0

e-122:583:98//AF086131

F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library *Oryza sativa* genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086

F-PLACE1002119//*Mus musculus* IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527

F-PLACE1002140//*Homo sapiens* DNA sequence from PAC 454M7 on chromosome X q25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162

F-PLACE1002150//*Plasmodium falciparum* MAL3P5, complete sequence.//0.12:408:61//AL034556

F-PLACE1002157//*Homo sapiens* BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539

F-PLACE1002163//*Homo sapiens* T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662

F-PLACE1002170//*Homo sapiens* Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805

F-PLACE1002171//*Mus musculus* interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244

F-PLACE1002205//*Drosophila melanogaster*; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:60//AC005720

F-PLACE1002213//HS\_3238\_B1\_G03\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965

F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800

F-PLACE1002256//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from contig 3-72, complete sequence.//0.022:458:59//AL010142

F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.  
21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene,  
EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, c  
omplete sequence.//3.5e-91:637:84//AL022324

F-PLACE1002319

F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U4995  
6

F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequ  
ence.//1.9e-127:487:93//AC004623

F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complet  
e sequence.//5.6e-05:474:59//AC005922

F-PLACE1002433//Drosophila melanogaster fidipidine gene, exons 1-7.//1.7  
e-11:613:58//AJ011928

F-PLACE1002437//M.musculus abc1 mRNA.//5.5e-62:452:85//X75926

F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (D  
G1098) gene, partial cds.//0.013:372:59//AF081801

F-PLACE1002450//HS\_3233\_A1\_G01\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey s  
equence.//3.1e-07:449:59//AQ204769

F-PLACE1002465

F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1  
.5e-110:720:85//U69262

F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems  
Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926

F-PLACE1002493//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cance  
r Institute Human PAC Library) complete sequence.//0.020:301:60//AC00606

0

F-PLACE1002499

F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927

F-PLACE1002514//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//3.7e-08:139:76//Z93930

F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256

F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:65//AC004774

F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575

F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314

F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//AC002523

F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443

F-PLACE1002591//H.sapiens mRNA for coronin.//7.2e-26:279:74//X89109

F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.0013:375:64//AC005537

F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785

F-PLACE1002625

F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:92//AC005281

F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete



cds.//3.6e-107:706:84//AF079765

F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180

F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726

F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723

F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL031273

F-PLACE1002772//HS\_3058\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567

F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259

F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927

F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey sequence.//1.3e-71:368:96//AQ075879

F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994

F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295

F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691

F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//9.3e-41:240:93//M27877

F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045

F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140

F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62//M10126

F-PLACE1002881//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200

F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//U19889

F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120

F-PLACE1002962

F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558

F-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605:93//AL023755

F-PLACE1002993//CIT-HSP-2338I16.TF CIT-HSP Homo sapiens genomic clone 2338I16, genomic survey sequence.//1.9e-13:100:95//AQ054760

F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980

F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551

F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088

F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829

F-PLACE1003045//H.sapiens CpG island DNA genomic MseI fragment, clone 47g6, forward read cpg47g6.ft1a.//0.0064:52:96//Z61200

F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 38

7P22, genomic survey sequence.//0.0031:249:63//B60158  
F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73/  
/U31875  
F-PLACE1003108  
F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), c  
omplete sequence.//6.3e-46:606:68//AC004219  
F-PLACE1003145  
F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-  
11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206  
F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 C  
ontains STS, GSS, complete sequence.//0.61:147:65//Z99495  
F-PLACE1003176//HS\_2255\_A2\_B01\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey s  
equence.//6.3e-09:137:76//AQ131934  
F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 u  
nordered pieces.//2.4e-138:791:90//AC005095  
F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B  
).//8.7e-06:728:57//X95276  
F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//  
7.5e-05:249:63//AC002466  
F-PLACE1003238//HS\_3239\_A2\_G02\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey s  
equence.//0.36:64:87//AQ209954  
F-PLACE1003249  
F-PLACE1003256  
F-PLACE1003258//HS\_3223\_A1\_G10\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey  
sequence.//1.4e-07:227:65//AQ190317  
F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 23

37F11, genomic survey sequence.//1.1e-13:97:95//AQ057429

F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of  
HPF1, -2, and -9.//2.3e-92:485:95//M27877

F-PLACE1003334

F-PLACE1003342

F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14  
unordered pieces.//1.0e-20:179:84//AC004951

F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 pro  
tein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715

F-PLACE1003361//Human Cosmid gl248a143 from 7q31.3, complete sequence.//  
1.9e-30:402:70//AC004095

F-PLACE1003366

F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-0  
7:378:60//AL034558

F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete  
sequence.//6.0e-18:471:61//AC005247

F-PLACE1003375

F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat e  
pithelium cancer , segment 10/10.//2.3e-157:779:96//AB020878

F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//  
1.2e-104:596:91//M83680

F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5,  
genomic survey sequence.//0.85:140:65//AQ268588

F-PLACE1003420//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388

F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0  
084:219:61//AF015470

F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA  
1) gene, complete cds.//1.3e-11:746:60//AF039401

F-PLACE1003493

F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//8.2e-41:379:78//AC002994

F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:247:76//AF064859

F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSS and a GSS.//4.4e-68:502:79//AL008729

F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336

F-PLACE1003537//Homo sapiens multispinning membrane protein mRNA, complete cds.//0.0054:322:59//U94831

F-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297

F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547

F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688

F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324

F-PLACE1003584//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-56, complete sequence.//0.0038:465:57//AL010230

F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT S

EQUENCE, 10 unordered pieces.//0.72:111:71//AC002557

F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476

F-PLACE1003596//Mus musculus integral membrane protein 1 (Itm1) mRNA, complete cds.//1.4e-54:685:68//L34260

F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-138:679:97//D83200

F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.//0.0074:265:63//AC005356

F-PLACE1003611//HS\_2198\_B1\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475

F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226

F-PLACE1003625//HS\_2238\_B2\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662

F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MKD10, complete sequence.//0.043:264:63//AB011478

F-PLACE1003669

F-PLACE1003704//RPCI11-23H21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830

F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305

F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1 p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920

F-PLACE1003723//HS\_2231\_A2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey

sequence.//1.2e-12:114:90//AQ235672

F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.  
//5.9e-33:592:67//M58297

F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.  
//3.6e-11:92:93//AF054840

F-PLACE1003762

F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014

F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160

F-PLACE1003783//HS\_2190\_A2\_C02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757

F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210

F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.//0.015:296:60//U52112

F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

F-PLACE1003850//P.falciparum histidine-rich protein genes.//0.39:330:60//M17028

F-PLACE1003858//Human DNA sequence from PAC 332011 on chromosome 1q24-1q25. Contains ESTs and STSS.//4.8e-07:461:59//Z98043

F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic

sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC  
005139

F-PLACE1003870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//  
9.4e-75:754:72//U58134

F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1  
unordered pieces.//6.7e-20:432:64//AC006030

F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:7  
02:67//D42108

F-PLACE1003892//RPCI11-24P17.TV RPCI-11 Homo sapiens genomic clone RPCI-  
11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPSH) mRNA, comple  
te cds.//2.7e-86:533:87//U49385

F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.  
4e-29:251:80//AF046591

F-PLACE1003923//Homo sapiens full length insert cDNA clone ZD40A05.//2.8  
e-25:316:70//AF086251

F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//  
AC005505

F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone  
2387C11, genomic survey sequence.//1.0:223:62//AQ239494

F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma  
-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequ  
ence.//6.7e-29:241:84//AC005954



F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:71  
9:86//AF032666

F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Re  
gion, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000  
052

F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences  
.//0.87:209:64//M34651

F-PLACE1004128//M.musculus G protein beta-subunit mRNA, complete cds.//2  
.5e-62:437:84//M63658

F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2  
C mRNA, complete cds.//1.4e-16:342:65//AF005355

F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p  
12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, com  
plete sequence.//1.2e-26:299:74//AL022099

F-PLACE1004161

F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ  
010071

F-PLACE1004197

F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precu  
sor, mRNA, complete cds.//4.0e-144:695:98//AF069493

F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6  
q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA rep  
eat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

F-PLACE1004256//HS\_2010\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey s  
equence.//1.5e-44:372:79//AQ252434

F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequen  
ce.//0.00011:349:63//AC005034

F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome

22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806  
 F-PLACE1004270//Human IgA C alpha 1 switch region (Sal).//1.7e-08:622:61  
 //L19121  
 F-PLACE1004274//H.sapiens CpG island DNA genomic MseI fragment, clone 18  
 g6, forward read cpgl8g6.ft1b.//8.6e-37:196:98//Z57691  
 F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, c  
 omplete cds.//6.0e-156:756:97//AF084830  
 F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone  
 : MPI7, complete sequence.//0.0060:635:57//AB011480  
 F-PLACE1004289//HS\_3023\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey s  
 equence.//2.4e-12:86:98//AQ094451  
 F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL0214  
 11  
 F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150  
 :797:94//Y11588  
 F-PLACE1004336//Drosophila melanogaster DNA sequence (P1 DS07968 (D117))  
 , complete sequence.//0.87:206:59//AC004267  
 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1  
 mRNA, complete cds.//5.9e-139:688:97//AF100153  
 F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4  
 .1e-81:498:89//AF046631  
 F-PLACE1004384//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653  
 F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:615:62//U  
 70855  
 F-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 u  
 nordered pieces.//9.2e-150:749:96//AC005027  
 F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete

sequence.//2.4e-08:129:76//AC005532

F-PLACE1004428//R.norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188

F-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283

F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739

F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//AC004954

F-PLACE1004467//HS\_2058\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700

F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//M27877

F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//3.3e-20:140:92//B80243

F-PLACE1004491//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709

F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150

F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.2e-146:699:98//AF040701

F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//1.4e-33:367:71//Z86001

F-PLACE1004518

F-PLACE1004548//Dictyostelium discoideum MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962

F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476

F-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931

F-PLACE1004629//Anolis carolinensis Brain-1 gene, complete cds.//0.00013:188:67//AB001868

F-PLACE1004645//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//0.66:337:60//Z95120

F-PLACE1004646//Rattus norvegicus retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.//1.1e-19:326:63//AF035673

F-PLACE1004658//H.sapiens CpG island DNA genomic MseI fragment, clone 55h1, forward read cpq55h1.ft1a.//2.4e-34:188:98//Z61632

F-PLACE1004664//Caenorhabditis elegans cosmid W10G6, complete sequence.//1.0:148:65//Z81140

F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//1.9e-101:182:95//U07561

F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//4.3e-109:625:91//AF035606

F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.9e-152:759:96//AB020860

F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSS and two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152

F-PLACE1004691//HS\_3044\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323

F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-2

6.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related  
, matrix associated, actin dependent regulator of chromatin, subfamily a  
, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains  
ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577

F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.0008  
1:428:59//Z98551

F-PLACE1004722//HS\_3052\_B1\_C10\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey  
sequence.//2.3e-05:104:75//AQ134959

F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 23  
65J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-PLACE1004740//RPCI11-58A7.TJ RPCI11 Homo sapiens genomic clone R-58A7,  
genomic survey sequence.//8.6e-26:522:65//AQ195766

F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mR  
NA, complete cds.//1.1e-112:711:86//AF061555

F-PLACE1004751

F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-  
171:828:97//AF084367

F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7./  
/4.2e-134:763:90//AJ001713

F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.  
21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical p  
rotein EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157

F-PLACE1004804

F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic  
sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//  
AC004710

F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complet  
e sequence.//9.8e-39:207:99//AC005921

F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613

F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849

F-PLACE1004827//HS\_2230\_A2\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313

F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825

F-PLACE1004838//HS\_3241\_A2\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740

F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//192819

F-PLACE1004868

F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.//0.14:465:59//Z97344

F-PLACE1004900

F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184

F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058

F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571

F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671

F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989

F-PLACE1004937

F-PLACE1004969

F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-pl4, complete sequence.//0.012:316:61//AC004843

F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26. 3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.7e-39:394:77//AL031073

F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833

F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:590:61//AE001373

F-PLACE1005026

F-PLACE1005027

F-PLACE1005046

F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867

F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148

F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//AF059569

F-PLACE1005077

F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//6.9e-29:253:77//AC004673

F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//AC002316

F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-146:734:96//AC005225

F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//AC004476

F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//

0.46:179:64//AC003081

F-PLACE1005111

F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcripti  
on control protein (BICP4) gene, complete cds.//0.00051:287:63//L14320

F-PLACE1005146//HS\_3071\_A1\_E03\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3071 Col=5 Row=I, genomic survey s  
equence.//7.4e-38:299:82//AQ103361

F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequenc  
e.//2.6e-44:346:82//AC002451

F-PLACE1005176

F-PLACE1005181//CIT-HSP-234005.TR CIT-HSP Homo sapiens genomic clone 234  
005, genomic survey sequence.//0.99:211:63//AQ054651

F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 235  
8N6, genomic survey sequence.//2.7e-07:80:90//AQ074445

F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//  
0.98:216:61//AC000061

F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42  
unordered pieces.//0.70:245:63//AC004965

F-PLACE1005243

F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.  
//0.00041:254:61//Z47812

F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4\_2g).//9.6e-33:177:98  
//Z70695

F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.  
6e-148:706:98//AB011182

F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cd  
s.//2.8e-15:737:60//M69183

F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, co  
mplete cds.//3.8e-111:728:84//M25757



F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence E RV-L pol gene, clone ERV-L Vole Cg14.//1.0:128:67//AJ233621

F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167

F-PLACE1005327//HS\_3080\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116

F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//AC004794

F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-114:237:92//AC000380

F-PLACE1005373

F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//AF017104

F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991

F-PLACE1005453//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y48A6, WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854

F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859

F-PLACE1005471//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581

F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191

F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021878

F-PLACE1005481//RPCI11-74L17.TJ RPCI11 Homo sapiens genomic clone R-74L1

7, genomic survey sequence.//0.37:403:57//AQ266885  
F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA  
, complete cds.//2.1e-67:325:99//AF080394  
F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-pl5, complete  
sequence.//0.015:403:61//AC005589  
F-PLACE1005526//H.sapiens CpG island DNA genomic MseI fragment, clone 9f  
1, reverse read cpg9f1.rtl1a.//3.6e-27:159:96//Z66485  
F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/  
28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038  
F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence.//6.5e-1  
8:234:72//AC004860  
F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic sur  
vey sequence.//1.2e-14:123:75//AL025925  
F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA ge  
ne.//0.43:209:66//X02354  
F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complet  
e sequence.//9.3e-113:536:97//AC004707  
F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomi  
c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:514:59/  
/AC005504  
F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds.//0  
.00056:289:63//AB014517  
F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete se  
quence.//1.2e-111:262:89//AC004126  
F-PLACE1005603  
F-PLACE1005611//F1605TFC IGF Arabidopsis thaliana genomic clone F1605, g  
enomic survey sequence.//2.0e-10:209:66//B98589  
F-PLACE1005623  
F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKI

NG DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840

F-PLACE1005639//HS\_3095\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence.//1.2e-05:220:63//AQ123022

F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//6.4e-150:721:98//AF083255

F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase.//1.3e-51:480:74//X59618

F-PLACE1005666//RPCI11-78015.TV RPCI11 Homo sapiens genomic clone R-78015, genomic survey sequence.//8.7e-05:243:62//AQ284667

F-PLACE1005698//Human membrane-associated lectin type-C mRNA.//1.9e-63:374:85//M98457

F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.69:633:57//AE001422

F-PLACE1005730//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//2.0e-24:286:74//AQ231147

F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.8e-55:621:71//U15635

F-PLACE1005755//HS\_2213\_A2\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=0, genomic survey sequence.//1.4e-25:290:75//AQ136844

F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//4.5e-40:297:70//M16200

F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5.//0.91:287:63//Y12517

F-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//5.0e-109:530:98//AC004827

F-PLACE1005803//HS\_3092\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey  
sequence.//2.4e-08:76:96//AQ103695

F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds  
./1.4e-126:636:96//AF027156

F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./  
/2.6e-154:739:98//AF065482

F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING  
DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150

F-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from contig 4-105, complete sequence.//0.00080:663:58//AL010283

F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//  
AC004153

F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.  
1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete  
sequence.//1.8e-46:278:85//AL031432

F-PLACE1005851

F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specifical  
ity factor.//5.0e-120:701:89//X75931

F-PLACE1005884//CIT-HSP-2333012.TR CIT-HSP Homo sapiens genomic clone 23  
33012, genomic survey sequence.//4.6e-78:385:98//AQ039226

F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+)  
mRNA, partial cds.//9.3e-16:638:57//U29892

F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRN  
A, complete cds.//1.0:178:65//U67136

F-PLACE1005921//M.musculus mRNA for immunity associated protein 38.//6.6  
e-17:614:59//Y08026

F-PLACE1005923//RPCI11-33G19.TJ RPCI-11 Homo sapiens genomic clone RPCI-  
11-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151

F-PLACE1005925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405

F-PLACE1005932

F-PLACE1005934//H.sapiens CpG island DNA genomic MseI fragment, clone 165g2, forward read cpgl65g2.ft1a.//8.3e-43:247:93//Z57153

F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence.//0.91:116:68//AL014719

F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236

F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081

F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070

F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925

F-PLACE1005968

F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866

F-PLACE1006002//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090

F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442

F-PLACE1006011//Mus musculus poly-(ADPriboseyl)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521

F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299

F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U

01139

F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906

F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200

F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023

F-PLACE1006129

F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597

F-PLACE1006143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015

F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:B2.//0.048:290:60//D85750

F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-105402 map 10q25, complete sequence.//3.2e-129:466:96//AC005661

F-PLACE1006164//HS\_3003\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence.//1.4e-70:388:93//AQ118200

F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//4.3e-78:385:86//AC005239

F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X14972

F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//3.9e-149:694:99//AF091433

F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//2.5e-16:283:70//AC003658

F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//2.2e-94:648:84//L25125

F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533:58//U75931

F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence.//0.0068:175:64//B19803

F-PLACE1006225//CIT-HSP-2335I23.TF CIT-HSP Homo sapiens genomic clone 2335I23, genomic survey sequence.//2.1e-19:149:90//AQ039880

F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.//0.51:290:58//U91327

F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452:96//AC004142

F-PLACE1006246//RPCI11-36I23.TK RPCI-11 Homo sapiens genomic clone RPCI-11-36I23, genomic survey sequence.//2.6e-31:176:97//AQ045400

F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791:98//AB014548

F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447

F-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320

F-PLACE1006318

F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454

F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VH5B32-D-JH2 region.//1.0:90:67//M55721

F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504

F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-0

5:625:57//AL034559

F-PLACE1006368//X.laevis mRNA for KLP2 protein.//3.0e-25:376:68//X94082

F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//2.0e-146:711:97//AC004232

F-PLACE1006382

F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-110:539:97//AF062085

F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.3e-23:463:68//AC005029

F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//AF069735

F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129

F-PLACE1006445//HS\_3071\_A1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ103347

F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496

F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA.//0.99:250:59//Z15118

F-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977

F-PLACE1006488//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744

F-PLACE1006492

F-PLACE1006506

F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083

F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2



C mRNA, complete cds.//2.6e-84:625:80//AF005355

F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.  
//0.00031:671:58//AL033510

F-PLACE1006540

F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete c  
ds.//6.0e-10:636:59//J03998

F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, comple  
te sequence.//9.8e-25:170:77//AC006044

F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eI  
F3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670

F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human  
BAC library) complete sequence.//0.98:514:59//AC004470

F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone w  
g2c3.//0.00079:206:62//X76589

F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete seque  
nce.//0.0012:576:57//AC004015

F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B  
).//0.0018:588:59//X95276

F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic  
sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC  
004688

F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltranf  
erase-I (b3GT1) gene, complete cds.//0.00011:184:64//AF029790

F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP)  
mRNA, complete cds.//0.0013:380:62//U67916

F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13.  
Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATE  
D P48 PROTEIN), ESTs and STS.//1.5e-78:520:86//Z98048

F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequ

ence.//1.9e-135:378:99//AC005626

F-PLACE1006760//CIT-HSP-2336013.TR CIT-HSP Homo sapiens genomic clone 23  
36013, genomic survey sequence.//0.018:147:66//AQ039246

F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of  
the complete sequence.//2.6e-08:823:58//AE001426

F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2  
unordered pieces.//0.043:252:65//AC005487

F-PLACE1006792//HS\_3165\_B1\_H01\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3165 Col=1 Row=P, genomic survey s  
equence.//1.4e-11:249:67//AQ149559

F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA,  
complete cds.//1.3e-12:155:80//M68513

F-PLACE1006800//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272

F-PLACE1006805//paramecium species 1,168 mt dna dimer: replication init.  
region.//9.1e-09:369:62//K00915

F-PLACE1006815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033

F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-1  
21:618:91//AC005230

F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, em  
bryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350

F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-0  
7:691:58//AL034559

F-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378

F-PLACE1006878

F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome; segmen  
t 138/162.//1.0:236:62//Z95120

F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672

F-PLACE1006904

F-PLACE1006917//H.sapiens CpG island DNA genomic MseI fragment, clone 79 g10, forward read cpg79g10.ft1a.//1.3e-21:131:98//Z63175

F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063

F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308

F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447

F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//U23921

F-PLACE1006961//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//1.6e-06:651:58//AJ223323

F-PLACE1006962//H.sapiens irlB mRNA.//7.1e-15:202:71//X63417

F-PLACE1006966//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594

F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188

F-PLACE1007014//Rattus norvegicus equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305

F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//5.1e-17:285:70//AC005777

F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat\*.//6.2e-131:775:89//Z82899

F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8

unordered pieces.//1.7e-143:675:99//AC004895

F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214\_0\_1, complete sequence.//1.3e-131:652:97//AC005224

F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6 . Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL021368

F-PLACE1007105//Mus musculus muskelin mRNA, complete cds.//4.1e-124:687:91//U72194

F-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139

F-PLACE1007112//HS\_2234\_B2\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801

F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112

F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt].//4.9e-15:386:62//S68151

F-PLACE1007178//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140

F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899

F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//2.8e-08:269:63//S74494

F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57:405:87//D50495

F-PLACE1007242//HS\_3006\_A1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ089443

F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9e-12:245:66//U49082

F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908

F-PLACE1007274//HS\_3003\_A1\_D08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154

F-PLACE1007276//Fugu rubripes GSS sequence, clone 014010aG11, genomic survey sequence.//0.0052:228:62//AL024982

F-PLACE1007282//F.rubripes GSS sequence, clone 019007aB3, genomic survey sequence.//0.024:289:58//AL011743

F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185:69//AC002492

F-PLACE1007301//Dictyostelium discoideum gene for TRFA, complete cds.//0.069:761:57//AB009080

F-PLACE1007317

F-PLACE1007342

F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120:567:98//AF096870

F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-59:613:75//AC005077

F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193:70//U88167

F-PLACE1007386

F-PLACE1007402//HS\_2170\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence.//5.6e-06:162:67//AQ125590

F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence.//1.6e-25:165:93//AF093772

F-PLACE1007416

F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973

F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds.//4.1e-17:374:64//AF041433

F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment.//8.1e-52:317:93//L40391

F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//0.0019:280:64//AL031117

F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 complete genomic sequence, complete sequence.//2.5e-24:362:71//AC002302

F-PLACE1007484

F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) mRNA, complete cds.//3.8e-14:293:63//AF017370

F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//4.6e-10:152:75//AL031311

F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//3.6e-139:477:98//AC004231

F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence.//0.0055:395:59//AF015461

F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome

b (cytb) genes, complete cds, and complete 9S rRNA gene and partial 12S rRNA gene.//0.0013:550:58//U11682

F-PLACE1007537//H.sapiens CpG island DNA genomic MseI fragment, clone 19 8g6, reverse read cpg198g6.rtl1a.//0.98:121:67//Z60280

F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508

F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds.//3 .1e-69:733:71//AB014561

F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule.//0.022:393 :61//X03240

F-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c lone 545L17, WORKING DRAFT SEQUENCE.//3.6e-114:565:97//AL031665

F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 23 71G14, genomic survey sequence.//2.0e-22:304:70//AQ111183

F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complet e sequence.//1.0:386:59//AC005245

F-PLACE1007621

F-PLACE1007632//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cance r Institute Human PAC Library) complete sequence.//1.0e-88:276:96//AC006 064

F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110:79//M2613 2

F-PLACE1007649

F-PLACE1007677//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c lone 968D22, WORKING DRAFT SEQUENCE.//1.2e-21:567:64//AL023755

F-PLACE1007688//Pseudorabies virus immediate-early gene.//2.2e-05:287:66 //X15120

F-PLACE1007690//Caenorhabditis elegans cosmid R07G3.//0.40:122:70//U2345 2

F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment.//0.85:117:71//L40483

F-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//0.0035:75:88//AL031662

F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-147:709:97//AF061243

F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MBB18, complete sequence.//1.0:510:58//AB005231

F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-136:516:89//U86698

F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728:98//AB014585

F-PLACE1007737//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.8e-22:806:60//AC005484

F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504

F-PLACE1007746//HS\_2268\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780

F-PLACE1007791//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//0.63:241:58//AL031749

F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879\_D\_6, complete sequence.//1.0e-120:743:87//AC005273

F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.0e-113:739:86//AC003658

F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438



F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//AL006903

F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP00010

F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309

F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey sequence.//0.015:279:61//AQ263271

F-PLACE1007877

F-PLACE1007897

F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//AB007956

F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//1.1e-59:310:81//AC003097

F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//2.1e-61:522:79//AC006157

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//AF084530

F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.5e-153:730:98//AF079529

F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//U13262

F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758

F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88//AF087695

F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.4e-163:786:98//AC005628

F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:84//L31840

F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719

F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3.//4.0e-07:251:64//Z68883

F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey sequence.//1.5e-30:166:99//B85883

F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondria. 1 gene encoding mitochondrial protein, partial cds.//7.5e-06:414:60//AF069163

F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867

F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586

F-PLACE1008132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111:93//Z82199

F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866:73//D14849

F-PLACE1008181//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727:56//AL034397

F-PLACE1008198//HS\_3073\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94:92//AQ171450

F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-162:791:97//AC005069

F-PLACE1008209

F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:  
174:66//M26332

F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP Homo sapiens genomic clone 233  
7B4, genomic survey sequence.//6.7e-28:165:95//AQ039317

F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:  
709:71//X92987

F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131:64//M2  
9123

F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome System  
s Human BAC Library) complete sequence.//0.011:96:73//AC005913

F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA,  
complete cds.//8.2e-86:672:77//AF078779

F-PLACE1008329//HS\_2027\_A1\_C06\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey  
sequence.//8.7e-09:116:81//AQ244432

F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequ  
ence.//2.2e-141:670:98//AC005176

F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 u  
nordered pieces.//2.1e-27:157:78//AC005000

F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.  
1e-137:659:98//AB014579

F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 231  
1C9, genomic survey sequence.//7.1e-08:398:60//AQ016352

F-PLACE1008369//HS\_2251\_B1\_A02\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey s  
equence.//2.1e-35:217:93//AQ066512

F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complet  
e sequence.//1.4e-11:403:64//AC005856

F-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681:99//AL034417

F-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257:96//AC004604

F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:98//D86326

F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688

F-PLACE1008424

F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//1.0e-88:331:84//AB020864

F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//U62317

F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349:94//AQ112479

F-PLACE1008455//HS\_2064\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589

F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:73//AC004526

F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210:99//B90014

F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//AB003494

F-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778:98//AL031778

F-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191:100//AF045555

F-PLACE1008532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257:70//Z93097

F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:71//AC004997

F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//0.66:263:64//Z99571

F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence.//1.1e-19:315:68//U73023

F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812:98//AB018334

F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.9e-09:198:71//AC005077

F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence.//0.68:568:59//AC005373

F-PLACE1008626//HS\_3221\_A2\_F03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence.//1.7e-13:147:82//AQ180967

F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//9.7e-98:586:88//Y12836

F-PLACE1008629//CIT-HSP-2012I4.TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence.//0.00085:203:66//B53732

F-PLACE1008630//Sequence 26 from Patent WO9517522.//9.7e-05:97:80//A45356

F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds.//1.4e-23:299:64//D38595

F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//1.1e-133:622:99//AF044333

F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence.//0.24:89:76//AQ060732

F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//1.4e-94:420:97//AF038406

F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence.//2.1e-70:349:98//AQ007199

F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.14:347:59//AC004260

F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//7.9e-25:244:71//AC003037

F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//4.5e-120:503:97//AF060543

F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.00026:370:61//AF001549

F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence.//3.3e-08:220:65//AQ036643

F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//1.7e-120:470:97//AF030933

F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//2.8e-87:504:89//AF032668

F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1 p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//4.0e-21:212:74//AL021920

F-PLACE1008854

F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//4.7e-77:477:84//Z82209

F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//3.4e-53:699:70//AC005539

F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds.//2.1e-06:16  
4:68//M63660

F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//6.  
4e-158:753:98//AB018308

F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180  
G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:400:63//AC00204  
2

F-PLACE1008934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022312

F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds.//  
4.3e-41:282:87//L15309

F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences  
.//5.9e-15:710:60//M34651

F-PLACE1009020//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey s  
equence.//1.9e-21:167:86//AQ253727

F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23  
Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat,  
GSS, complete sequence.//4.1e-152:763:97//AL031117

F-PLACE1009039//HS\_2034\_A2\_F08\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey  
sequence.//0.17:252:59//AQ230137

F-PLACE1009045//HS\_3185\_B2\_B03\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey s  
equence.//1.9e-34:260:86//AQ172861

F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5  
'flank and exon 1.//4.7e-70:463:80//D00766

F-PLACE1009050//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Canc  
er Institute Human PAC library) complete sequence.//0.63:280:61//AC00424

1

F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X)  
, complete CDS.//5.9e-113:725:85//AJ005073

F-PLACE1009090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 1045J21, WORKING DRAFT SEQUENCE.//9.1e-27:222:84//AL021919

F-PLACE1009091//Homo sapiens clone DJ0968I16, complete sequence.//0.027:  
630:58//AC006016

F-PLACE1009094

F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds.//2.1  
e-85:726:76//M36515

F-PLACE1009110

F-PLACE1009111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 138B7, WORKING DRAFT SEQUENCE.//6.0e-12:362:64//Z98752

F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3  
(XRCC3) mRNA, complete cds.//3.4e-138:671:97//AF035586

F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-23:718  
:59//D25215

F-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRA  
FT SEQUENCE.//6.1e-142:684:98//AJ011929

F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/  
28, WORKING DRAFT SEQUENCE.//4.3e-36:227:77//AP000031

F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3' region invol  
ved in DNA excision repair.//1.0:173:60//X52222

F-PLACE1009166

F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence.//4.0e-  
35:257:85//AC002070

F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Sys  
tems Human BAC Library) complete sequence.//2.9e-19:288:72//AC004805

F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone



: MHJ24, complete sequence.//0.053:388:60//AB008266  
F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds.//1.8e-50:317:89//AF061242  
F-PLACE1009190//RPCI11-81N5.TJ RPCI11 Homo sapiens genomic clone R-81N5, genomic survey sequence.//0.91:114:67//AQ281881  
F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey sequence.//2.8e-44:175:83//AQ262198  
F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotein.//1.1e-106:495:88//X63203  
F-PLACE1009246//HS\_3058\_B1\_A06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, genomic survey sequence.//0.10:175:68//AQ185945  
F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.8e-94:575:89//U47024  
F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region.//0.0017:350:62//U23862  
F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds.//3.0e-06:411:59//U83192  
F-PLACE1009328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191P20, WORKING DRAFT SEQUENCE.//5.7e-138:830:86//AL034399  
F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain.//0.071:253:62//D87015  
F-PLACE1009338//RPCI11-74N24.TV RPCI11 Homo sapiens genomic clone R-74N24, genomic survey sequence.//2.4e-34:180:100//AQ268811  
F-PLACE1009368  
F-PLACE1009375  
F-PLACE1009388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1014D13, WORKING DRAFT SEQUENCE.//2.0e-37:288:84//AL022311  
F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds.//4.

3e-78:730:74//M27878

F-PLACE1009404//Smd homolog [mice, liver, mRNA Partial, 199 nt] .//0.16:9  
5:71//S71494

F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complet  
e sequence.//1.6e-150:701:99//AC005919

F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence.//2.9  
e-73:442:88//AF046700

F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segmen  
t 148/162.//0.012:582:56//AL022022

F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230)  
mRNA, complete cds.//4.6e-21:146:93//AF012872

F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence.//2.  
9e-31:264:81//AF046660

F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84//1305  
36

F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, co  
mplete sequence.//1.9e-142:704:97//AC004531

F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence.//2  
.2e-09:235:68//AC004601

F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete  
sequence.//2.9e-83:171:92//U91321

F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22  
q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytoh  
esin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a g  
ene coding for a Leucine rich protein. Contains ESTs, STSS and GSSs, com  
plete sequence.//3.8e-69:175:92//Z94160

F-PLACE1009539//Mus musculus synaptojanin 2 isoform alpha mRNA, complete  
cds.//7.0e-26:237:78//AF041862

F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12

.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//3.1e-10:126:79//AL031587

F-PLACE1009571//RPCI11-60K12.TK RPCI11 Homo sapiens genomic clone R-60K12, genomic survey sequence.//1.4e-05:68:91//AQ195869

F-PLACE1009581

F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence.//6.6e-19:309:70//AC003959

F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-09:485:59//AF016049

F-PLACE1009607//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824

F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.017:655:57//AC004157

F-PLACE1009621

F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genomic survey sequence.//2.7e-15:100:98//B33248

F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.63:130:67//AC005308

F-PLACE1009639//S.pombe chromosome II cosmid c24E9.//0.86:509:58//AL021816

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.4e-171:816:98//AB011159

F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.4e-67:437:87//AC005177

F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5e-147:  
701:98//AF062534

F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//1.5e-9  
8:228:100//AC006011

F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//  
2.2e-130:736:91//AC000109

F-PLACE1009731//M.musculus mRNA for immunity associated protein 38.//1.1  
e-13:311:64//Y08026

F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2e-125:6  
02:98//AF046024

F-PLACE1009794

F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25  
-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3,  
EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein  
Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part o  
f a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C  
. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1  
.3e-73:271:84//AL030996

F-PLACE1009845

F-PLACE1009861//B.tauris cathepsin B mRNA, 3' end.//0.00023:147:65//M646  
20

F-PLACE1009879//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397

F-PLACE1009886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427

F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, g  
enomic survey sequence.//0.0044:232:60//AQ251431

F-PLACE1009908//S.pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z693  
69

F-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//5.9e-48:304:87//M63005

F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-201104, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529

F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0027C22r, genomic survey sequence.//0.98:220:67//AQ272066

F-PLACE1009935//Sequence 16 from patent US 5552281.//0.030:152:67//I25655

F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-12:322:67//AC006026

F-PLACE1009971

F-PLACE1009992//HS\_3178\_B1\_F04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence.//4.9e-23:142:95//AQ150311

F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00019:231:64//Z81029

F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//7.9e-87:552:80//U48288

F-PLACE1010023

F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-101:181:98//AL031775

F-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//2.3e-136:689:95//X84692

F-PLACE1010069//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./

/1.8e-166:792:98//AF065482  
 F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//  
 7.5e-13:203:77//D25540  
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.  
 0e-152:727:98//AB007925  
 F-PLACE1010089//HS\_3111\_A1\_E08\_T7 CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=3111 Col=15 Row=I, genomic survey  
 sequence.//4.8e-07:124:78//AQ101268  
 F-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//1.2e-108:700:85/  
 /X64411  
 F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic  
 sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//  
 AC005506  
 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete  
 cds.//3.8e-25:728:60//AF059569  
 F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22.//  
 6.5e-25:488:63//Z93928  
 F-PLACE1010134//S.pombe chromosome I cosmid c29B12.//1.9e-13:238:67//Z99  
 164  
 F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-83:409:9  
 8//AJ222636  
 F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 23  
 81F24, genomic survey sequence.//1.5e-28:163:98//AQ196757  
 F-PLACE1010181//Homo sapiens PAC clone DJ1139I01 from Xq23, complete seq  
 uence.//2.4e-15:197:72//AC004973  
 F-PLACE1010194//Ictalurus punctatus tumor supressor p53 mRNA, complete c  
 ds.//3.0e-14:181:74//AF074967  
 F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13  
 829

F-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033377

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5  
.8e-145:693:97//AB007917

F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic  
sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//  
AC004710

F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence./  
/0.00040:231:64//Z81029

F-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park  
Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70/  
/AC004464

F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome  
1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS,  
CA repeat, complete sequence.//3.5e-10:185:67//AL031005

F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.  
3, complete sequence.//0.010:524:58//Z84468

F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 23  
35J21, genomic survey sequence.//9.1e-90:448:97//AQ041837

F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome./  
/2.8e-08:384:64//L06178

F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequ  
ence.//4.1e-21:141:92//B38252

F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome; segmen  
t 155/162.//0.94:398:57//AL022121

F-PLACE1010364//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985

F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete

sequence.//0.066:88:76//AC004675  
F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 23  
67K17, genomic survey sequence.//2.4e-71:454:88//AQ076825  
F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//7  
.5e-134:722:93//AF003927  
F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete c  
ds.//2.2e-150:702:99//AF039081  
F-PLACE1010492  
F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82  
695  
F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145:684:98//AR0  
16417  
F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.  
22-12.2. Contains STSS and GSSs, complete sequence.//1.0:283:61//AL03167  
7  
F-PLACE1010562//RPCI11-65I16.TK RPCI11 Homo sapiens genomic clone R-65I1  
6, genomic survey sequence.//0.017:216:67//AQ200831  
F-PLACE1010579//Homo sapiens full length insert cDNA YI23D12.//3.9e-19:1  
47:89//AF075014  
F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEA  
D box family mRNA, complete cds.//6.4e-96:559:89//L25125  
F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14  
p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186  
F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic  
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC  
005308  
F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-0  
7:378:60//AL034558  
F-PLACE1010624//Streptomyces coelicolor cosmid 5A7.//1.4e-05:518:61//AL0



31107

F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846

F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//2.5e-17:187:80//AC004682

F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence.//0.21:159:64//AB016872

F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069

F-PLACE1010661

F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960

F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376

F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583

F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678

F-PLACE1010739//HS\_2013\_B2\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864

F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609

F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//4.7e-45:235:99//AC005921

F-PLACE1010771//M.musculus HCNGP mRNA.//1.6e-135:801:88//X68061

F-PLACE1010786//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-15, complete sequence.//0.35:334:60//AL010221

F-PLACE1010800//RPCI11-79H17.TV RPCI11 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252

F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.

6e-30:693:63//AC004384

F-PLACE1010811//RPCI11-51N5.TK RPCI11 Homo sapiens genomic clone R-51N5,  
genomic survey sequence.//8.3e-11:142:78//AQ052380

F-PLACE1010833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283

F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229

F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of  
hepatocellular colorectal and non-small cell lung cancer , segment 11/11  
..//1.4e-94:422:95//AB020868

F-PLACE1010870//M.musculus mRNA for ZT3 zinc finger factor.//1.3e-93:530  
:90//Z67747

F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.  
1e-147:694:98//AB011182

F-PLACE1010891

F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Loc  
us), complete sequence.//3.9e-26:394:68//AC003997

F-PLACE1010900

F-PLACE1010916//HS\_2242\_A1\_C04\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2242 Col=7 Row=E, genomic survey s  
equence.//1.0e-78:391:97//AQ146687

F-PLACE1010917

F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic  
sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC00  
4688

F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.  
5e-138:653:98//AB011126

F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds./  
/5.6e-90:437:98//AF064243

F-PLACE1010944//Homo sapiens full length insert cDNA clone ZD38E12.//1.4

e-09:208:68//AF086247

F-PLACE1010947

F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey sequence.//2.1e-29:190:91//B98965

F-PLACE1010960//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//0.00074:421:60//AL010226

F-PLACE1010965//CIT-HSP-2386K24.TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey sequence.//1.8e-84:412:99//AQ240696

F-PLACE1011026//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.00037:257:64//AL008972

F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBNL H176), complete sequence.//3.8e-06:315:65//AC005348

F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U70669

F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20636

F-PLACE1011054//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 981L23, WORKING DRAFT SEQUENCE.//3.8e-27:196:84//AL031686

F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds.//5.4e-06:182:67//U77049

F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:100//S75548

F-PLACE1011090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//5.1e-80:479:89//AL031687

F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//2.3e-24:192:84//L14684

F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249

F-PLACE1011133//T7E9-T7.1 TAMU Arabidopsis thaliana genomic clone T7E9,

genomic survey sequence.//0.010:345:60//B19698  
 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 23  
 75J10, genomic survey sequence.//0.00013:95:76//AQ109305  
 F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, comp  
 lete sequence.//3.7e-111:692:87//AC004893  
 F-PLACE1011165//H.sapiens galactokinase (GK2) mRNA, complete cds.//8.4e-  
 31:194:92//M84443  
 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-249B10,  
 complete sequence.//3.1e-43:447:72//AC002288  
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransfe  
 rase mRNA, complete cds.//3.3e-124:584:99//AF038664  
 F-PLACE1011214//HS\_2046\_A2\_B01\_MR CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=2046 Col=2 Row=C, genomic survey s  
 equence.//2.0e-39:346:81//AQ305965  
 F-PLACE1011219  
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone  
 2513F18, genomic survey sequence.//2.4e-20:119:100//AQ279801  
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.  
 4e-146:675:99//AB011101  
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequ  
 ence.//1.7e-42:212:84//AC005014  
 F-PLACE1011273//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
 \* from clone Y37D8, WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819  
 F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-1  
 1-16P9, genomic survey sequence.//8.0e-08:66:98//B81770  
 F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), c  
 omplete sequence.//0.027:135:67//AC004647  
 F-PLACE1011310//H.sapiens CpG island DNA genomic MseI fragment, clone 53  
 c10, reverse read cpg53c10.rtlb.//1.4e-05:57:100//Z61496

F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290

F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265

F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388\_F\_14, complete sequence.//2.4e-38:186:83//AC005375

F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:689:63//AF023919

F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310

F-PLACE1011399//paramecium species 7,325 mt dna dimer: replication init. region.//0.00011:255:63//K00919

F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:62//AJ006996

F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:98//AB011102

F-PLACE1011452//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.1e-53:557:73//AJ011929

F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//3.5e-71:498:80//AC004605

F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:99//AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:675:99//AF065482

F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA.//1.0:448:59//J00964

F-PLACE1011503

F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//3.8e-147:692:99//AC004968

F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//0.00036:296:61//X83546

F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence.//1.1e-38:315:82//AC004984

F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds.//1.3e-65:268:86//AF054180

F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.0e-82:188:96//AC004477

F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214\_0\_1, complete sequence.//1.8e-153:752:97//AC005224

F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660

F-PLACE1011643//Alcaligenes eutrophus phaP gene.//0.16:466:59//X85729

F-PLACE1011646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383

F-PLACE1011649

F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062

F-PLACE1011664//D.melanogaster crn mRNA.//1.1e-52:650:68//X58374

F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507

F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:127:71//AL008719

F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487

F-PLACE1011725

F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737

F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157

F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004003

F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22D17, genomic survey sequence.//2.7e-114:611:93//AQ008944

F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330

F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147

F-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.5e-141:678:98//AC004478

F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152

F-PLACE1011891//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392

F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969

F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400

F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617

F-PLACE1011962//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369

F-PLACE1011964//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799

F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529

F-PLACE1011995//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC006054

F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.2e-146:690:98//AB018256

F-PLACE2000003//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//1.7e-62:293:88//AC005837

F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//1.4e-116:261:91//AC006057

F-PLACE2000007

F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//AC005578

F-PLACE2000014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574

F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:316:81//AC005069

F-PLACE2000017//HS\_3042\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074

F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556

F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638

F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62/



/Y08913

F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//AF041082

F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:489:90//L08505

F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626

F-PLACE2000050//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//AC003101

F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey sequence.//1.1e-05:89:83//AQ059010

F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457

F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219

F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-16:119:93//AC005910

F-PLACE2000100//HS\_3184\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004

F-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848

F-PLACE2000111//Homo sapiens DNA, trinucleotide repeats region.//1.0:200:64//AB018491

F-PLACE2000115

F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//6.2e-43:362:80//AC004531

F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapiens genomic clone R-79F1

5, genomic survey sequence.//5.4e-35:206:94//AQ284166  
 F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence.//2.7e-12:814:59//AC002070  
 F-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//3.6e-165:799:97//AL020995  
 F-PLACE2000164//Canine histamine H2 receptor gene, complete cds.//0.10:392:56//M32701  
 F-PLACE2000170  
 F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence.//3.9e-91:552:88//AC006005  
 F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCR L2-GGT Region, complete sequence.//0.98:201:64//AC004032  
 F-PLACE2000187  
 F-PLACE2000216  
 F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey sequence.//0.00039:325:58//B75888  
 F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence.//7.5e-55:237:78//AC003003  
 F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//2.4e-92:236:94//AC005902  
 F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//1.4e-32:331:78//AL031577  
 F-PLACE2000274//Anthocidaris crassispina mRNA for B2HC, partial cds.//8.5e-48:765:66//AB012308  
 F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//8.3e-08:662:58//U52064  
 F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.4e-08:95:81//AC006021

F-PLACE2000317//HS\_3183\_B2\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence.//2.5e-71:346:99//AQ172747

F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.7e-14:402:65//AC004952

F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.//4.5e-77:555:82//AF026554

F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds.//1.8e-14:259:71//U66829

F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543, , and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//6.0e-34:376:74//AC003006

F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey sequence.//8.4e-21:288:69//AQ013849

F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence.//5.0e-114:692:80//U49973

F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.38:356:58//AC005182

F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey sequence.//0.064:132:68//AQ051776

F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.6e-130:776:88//AC003658

F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//5.4e-113:808:83//AC005909

F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene.//0.87:286:63//X06967

F-PLACE2000399

F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2

.9e-59:532:68//Z36238

F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.//0.44:553:56//U89984

F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4e-56:303:86//M13792

F-PLACE2000425//HS\_3047\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=0, genomic survey sequence.//2.8e-42:224:97//AQ126949

F-PLACE2000427

F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.1e-19:363:67//AC005821

F-PLACE2000435//HS\_3036\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999

F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:550:62//AL021492

F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:80//AC006025

F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-05:330:63//AC002300

F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.7e-168:816:97//AC005740

F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//4.3e-33:296:79//AC002037

F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//3.4e-59:598:74//AC005057

F-PLACE30000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602

F-PLACE30000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713

:69//U49187

F-PLACE3000020//R.norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075

F-PLACE3000029

F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267

F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-17:250:74//AC005368

F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006

F-PLACE3000119//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670

F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668

F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//1.8e-48:330:79//AC005695

F-PLACE3000136

F-PLACE3000142//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520

F-PLACE3000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662

F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSS and GSSs, complete sequence.//5.1e-37:305:81//AL031053

F-PLACE3000148//Homo sapiens chromosome Y, clone 475I1, complete sequence.//4.7e-32:766:63//AC004474

F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//7.4e-173:822:98//AC005277

F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//AC003682

F-PLACE3000157

F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500

F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey sequence.//0.080:259:59//B50878

F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//9.8e-158:749:98//AC006130

F-PLACE3000194

F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey sequence.//1.4e-08:164:68//AL003352

F-PLACE3000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207

F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//AC005013

F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982

F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//AC004086

F-PLACE3000220//RPCI11-54B4.TV RPCI11 Homo sapiens genomic clone R-54B4, genomic survey sequence.//2.4e-36:381:76//AQ082056

F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-135:721:91//AC005231

F-PLACE3000226

F-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. C ontains ESTs, STSS and genomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046

F-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169

F-PLACE3000254//Ateline herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424

F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//1.8e-21:350:68//AF001548

F-PLACE3000276//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sper m Libra ry D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147

F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequ ence.//1.6e-138:650:99//AC005328

F-PLACE3000310

F-PLACE3000320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c lone 423B22, WORKING DRAFT SEQUENCE.//1.9e-41:379:77//AL034379

F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complet e sequence.//3.3e-35:419:68//AC005822

F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 23 47D24, genomic survey sequence.//2.7e-20:119:99//AQ061543

F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bch I (bchI) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, part ial cds.//0.99:310:58//AF017642

F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Par k Cancer Institute Human PAC Library) complete sequence.//7.5e-159:752:9

8//AC006055

F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TA01 mRNA, complete cds.//2.3e-107:592:92//AF084205

F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//2.1e-37:480:70//Z83732

F-PLACE3000353

F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.00011:373:60//AC005969

F-PLACE3000363

F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007

F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSS. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545

F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//AC005154

F-PLACE3000399//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630

F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239

F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.8e-25:292:73//AC006023

F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence.//1.1e-10:154:74//AQ008761

F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.9e-41:515:72//AC005701

F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific co



smid Homo sapiens genomic clone cSRL-179E11, genomic survey sequence.//2  
 .8e-91:540:89//B03443  
 F-PLACE3000413  
 F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8,  
 genomic survey sequence.//0.0018:664:55//B11305  
 F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1  
 -27.3 Contains GSS, STS, complete sequence.//1.1e-16:284:70//AL022719  
 F-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 469D22, WORKING DRAFT SEQUENCE.//3.6e-146:732:96//AL031284  
 F-PLACE3000475//HS\_2164\_A2\_H10\_MF CIT Approved Human Genomic Sperm Libra  
 ry D Homo sapiens genomic clone Plate=2164 Col=20 Row=0, genomic survey  
 sequence.//1.5e-07:159:71//AQ132983  
 F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Conta  
 ins ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STS  
 s.//2.9e-11:213:70//Z83843  
 F-PLACE4000009//Sequence 93 from patent US 5616500.//9.9e-08:692:60//I39  
 845  
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//1.  
 1e-116:331:100//AB018352  
 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, c  
 omplete sequence.//5.0e-05:244:63//AC004131  
 F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems  
 Human BAC Library) complete sequence.//1.2e-37:385:74//AC005926  
 F-PLACE4000052//M.musculus abc1 mRNA.//1.5e-110:671:88//X75926  
 F-PLACE4000063  
 F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter r  
 egion related to EC cell differentiation.//3.7e-12:114:85//X74311  
 F-PLACE4000093//CIT-HSP-238OK5.TF CIT-HSP Homo sapiens genomic clone 238  
 OK5, genomic survey sequence.//0.11:245:60//AQ108342

F-PLACE4000100//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//2.9e-19:384:65//AL031848

F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds.//1.2e-145:684:99//AB007931

F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//3.7e-62:541:78//AF091234

F-PLACE4000129

F-PLACE4000131//HS\_3139\_B2\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence.//2.3e-14:221:70//AQ183207

F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence.//0.28:412:58//AL031622

F-PLACE4000156//Human zinc finger protein ZNF136.//7.2e-88:764:76//U09367

F-PLACE4000192

F-PLACE4000211

F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence.//1.2e-14:177:76//B17158

F-PLACE4000230//Mus musculus semaphorin VIA mRNA, complete cds.//9.8e-116:662:89//AF030430

F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//5.2e-54:363:70//AC003973

F-PLACE4000247

F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.0053:229:65//AC004673

F-PLACE4000252

F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.0e-25:191:87//Z70200

F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.6e-23:314:71//AF084259

F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//5.5e-122:734:88//AF032667

F-PLACE4000270

F-PLACE4000300

F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds.//1.4e-21:135:96//L34075

F-PLACE4000323//HS\_2165\_B1\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-08:170:71//AQ125036

F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//2.8e-06:311:63//M10296

F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.014:252:60//AE001401

F-PLACE4000367

F-PLACE4000369

F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661

F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649

F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:68//AF054088

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540

F-PLACE4000411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984

F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200

F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequ  
ence.//0.070:47:100//B41346

F-PLACE4000450

F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete se  
quence.//2.3e-07:273:65//AC005065

F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complet  
e sequence.//4.1e-34:351:70//AC005821

F-PLACE4000489//HS\_3012\_B1\_G05\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey s  
equence.//2.0e-36:220:92//AQ095537

F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Can  
cer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC0  
05865

F-PLACE4000521//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRA  
FT SEQUENCE.//1.6e-163:770:98//AJ011929

F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C,  
partial cds.//4.0e-124:686:90//U47645

F-PLACE4000548

F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:43  
5:59//X12747

F-PLACE4000581

F-PLACE4000590//Homo sapiens chromosome Y, clone 475I1, complete sequenc  
e.//3.6e-20:747:59//AC004474

F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence./  
/5.6e-16:326:65//Z78418

F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, comp  
lete sequence.//1.7e-163:785:97//AC005281

F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3

unordered pieces.//8.7e-74:707:74//AC006039

F-PLACE4000650

F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267

F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816

F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577

F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554

F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616

F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797

F-THYRO1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561

F-THYRO1000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637

F-THYRO1000034//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353

F-THYRO1000035//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:303:83//AC004383

F-THYRO1000040

F-THYRO1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383

F-THYRO1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.

7e-84:722:77//AB014557

F-THYR01000085

F-THYR01000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2  
013L16, genomic survey sequence.//0.31:186:61//B60606

F-THYR01000107

F-THYR01000111//Human genomic DNA sequence from clone 30801 on chromosom  
e Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:  
690:87//Z93403

F-THYR01000121//Rattus norvegicus CTD-binding SR-like protein ra8 mRNA,  
complete cds.//1.4e-127:816:85//U49055

F-THYR01000124//H.sapiens CpG island DNA genomic MseI fragment, clone 72  
a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724

F-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e  
-154:732:98//AF087142

F-THYR01000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequ  
ence.//3.7e-39:315:82//AC002096

F-THYR01000156//Human DNA sequence from clone 113J7 on chromosome Xp11.2  
2-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an  
STS, complete sequence.//1.2e-21:335:71//AL023574

F-THYR01000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7,  
complete sequence.//8.4e-52:301:88//AC002331

F-THYR01000173//Mouse clathrin-associated protein (AP47) mRNA, complete  
cds.//4.0e-89:821:74//M62419

F-THYR01000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207

F-THYR01000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57  
//X06214

F-THYR01000190//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complet  
e sequence.//0.38:184:64//AC005746

F-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.  
5e-174:805:99//AJ005698

F-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1  
.2e-86:616:84//AB014552

F-THYR01000206//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Lib  
rary D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey s  
equence.//0.51:331:63//AQ099134

F-THYR01000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic  
sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC  
004157

F-THYR01000241//Gallus gallus genome fragment with pentamer tandem repea  
ts.//0.43:191:62//X00186

F-THYR01000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156

F-THYR01000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Par  
k Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//A  
C006055

F-THYR01000270

F-THYR01000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664

F-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179  
:848:98//AB016068

F-THYR01000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complet  
e cds.//1.0e-44:331:83//AF036894

F-THYR01000327//Homo sapiens autocrine motility factor receptor (AMFR) m  
RNA, complete cds.//5.7e-112:641:91//L35233

F-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.  
2e-162:763:98//AB018333

F-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds  
.//2.2e-32:177:84//U29091

F-THYRO1000368//Caenorhabditis elegans cosmid W09G3, complete sequence./  
/0.97:206:60//Z82080

F-THYRO1000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668

F-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019

F-THYRO1000394//HS\_2061\_A2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672

F-THYRO1000395//Drosophila melanogaster ring canel protein and ORF2 mRNA, complete cds.//4.3e-15:512:59//L08483

F-THYRO1000401  
3.2e-116:504:80//AF051908

F-THYRO1000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308

F-THYRO1000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573

F-THYRO1000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229

F-THYRO1000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196

F-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740

F-THYRO1000501//H.sapiens Staf50 mRNA.//9.8e-74:615:77//X82200

F-THYRO1000502//Human DNA sequence from PAC 436M11 on chromosome Xp22:11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.0



76:380:59//Z94056

F-THYRO1000505

F-THYRO1000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563

F-THYRO1000569//HS\_2178\_B2\_E03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499

F-THYRO1000570

F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//AF075587

F-THYRO1000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323

F-THYRO1000602//HS\_3037\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057

F-THYRO1000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777

F-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546

F-THYRO1000637//Human DNA sequence from clone 91J24 on chromosome 6q24 C contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474

F-THYRO1000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559

F-THYRO1000658//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//1.1e-68:468:84//AC005696

F-THYRO1000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874

F-THYRO1000666//Mus musculus mRNA for motor domain of KIF9, partial cds.

//4.7e-58:367:87//AB001437

F-THYRO1000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778

F-THYRO1000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PR GFR3 genes.//6.6e-13:236:69//AJ010317

F-THYRO1000699//RPCI11-50D4.TK RPCI11 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641

F-THYRO1000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053

F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320

F-THYRO1000734//HS\_3233\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143

F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871

F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523

F-THYRO1000777//S.griseus str0 gene and sts gene cluster.//8.2e-05:625:59//Y08763

F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373

F-THYRO1000787//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986

F-THYRO1000793

F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422

F-THYRO1000805//Homo sapiens Xp21 PAC RPCI1-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43

:677:66//AC004468

F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914

F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053

F-THYRO1000843

F-THYRO1000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782

F-THYRO1000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:64//AF008573

F-THYRO1000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477

F-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720

F-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015

F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529

F-THYRO1000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836

F-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229

F-THYRO1000952

F-THYRO1000974//HS\_3238\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//2.4e-26:154:96//AQ219846

F-THYRO1000975//Plasmodium falciparum TopoII gene.//0.32:491:58//X79345

F-THYRO1000983//Mv9A3 exon amplification products from BACs in Mv9A region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ0

10457

F-THYRO1000984//CIT-HSP-2167017.TR CIT-HSP Homo sapiens genomic clone 2167017, genomic survey sequence.//0.00015:186:66//B91313

F-THYRO1000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588

F-THYRO1001003

F-THYRO1001031//Homo sapiens chromosome 17, clone hRPC.859\_0\_20, complete sequence.//1.1e-55:543:72//AC003695

F-THYRO1001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799

F-THYRO1001062//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320

F-THYRO1001093//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//4.9e-34:353:76//AC006241

F-THYRO1001100//Human DNA-binding protein mRNA, 3' end.//1.1e-72:742:74//L14787

F-THYRO1001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522

F-THYRO1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 671014, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595

F-THYRO1001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996

F-THYRO1001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486

F-THYRO1001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178

F-THYRO1001173

F-THYRO1001177//Human pigment epithelium-derived factor gene, complete c

ds.//1.9e-42:250:86//U29953

F-THYRO1001189//HS\_3171\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330

F-THYRO1001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925

F-THYRO1001213//, complete sequence.//1.7e-45:257:84//AC005300

F-THYRO1001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036

F-THYRO1001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496

F-THYRO1001287//Drosophila melanogaster cosmid clone 86E4.//9.6e-49:586:69//AL021086

F-THYRO1001290//HS\_2045\_B1\_H09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237

F-THYRO1001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693

F-THYRO1001320//Homo sapiens Chromosome 22q11.2 PAC Clone p\_n5 In BCRL2-GGT Region, complete sequence.//1.1e-88:672:82//AC002472

F-THYRO1001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114

F-THYRO1001322//HS\_3205\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025

F-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288

F-THYRO1001363//Homo sapiens PAC clone DJ0845I21 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:74//AC004905

F-THYR01001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10 q25, complete sequence.//7.6e-168:821:97//AC005660

F-THYR01001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607

F-THYR01001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//AC005239

F-THYR01001403//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//3.6e-70:360:86//AC005845

F-THYR01001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852

F-THYR01001406//Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.//1.0e-91:631:82//AF064635

F-THYR01001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//AC006126

F-THYR01001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AJ002553

F-THYR01001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.0:98:70//AC000384

F-THYR01001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265

F-THYR01001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-42:357:80//AC006001

F-THYR01001487//H.sapiens DNA sequence.//0.92:160:64//Z22449

F-THYR01001534//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-47:266:80//AC004666

F-THYR01001537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.3e-79:479:89//AL031687

F-THYR01001541//Human DNA sequence from clone 399M14 on chromosome Xq26.

1-26.3. Contains ESTs, an STS and GSSs, complete sequence.//0.0034:106:77//Z96074

F-THYR01001559//Rattus norvegicus simple sequence repeat D18Mco6.//1.6e-09:351:63//AF006056

F-THYR01001570//RPCI11-49B23.TJ RPCI11 Homo sapiens genomic clone R-49B23, genomic survey sequence.//1.4e-65:384:91//AQ052105

F-THYR01001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572

F-THYR01001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-THYR01001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//8.7e-145:779:93//AL023808

F-THYR01001602//Homo sapiens chromosome 17, clone hRPK.786\_0\_4, complete sequence.//2.9e-26:393:68//AC005863

F-THYR01001605//Dictyostelium discoideum filopodin (tala) gene, complete cds.//0.0012:436:58//U14576

F-THYR01001617//Homo sapiens full length insert cDNA clone ZD69D05.//8.6e-43:342:82//AF086381

F-THYR01001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//6.2e-15:318:66//AC004950

F-THYR01001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//AC004827

F-THYR01001661

F-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//AJ225089

F-THYR01001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071

F-THYR01001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857

F-THYR01001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:75//AC004745

F-THYR01001721//, complete sequence.//9.9e-134:770:91//AC005500

F-THYR01001738//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 355C18, WORKING DRAFT SEQUENCE.//0.99:163:61//AL022327

F-THYR01001745

F-THYR01001746

F-THYR01001772//HS\_3069\_B1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021

F-THYR01001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626

F-THYR01001809

F-THYR01001828//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526

F-THYR01001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//AC003664

F-THYR01001895

4.4e-13:248:68//AB012576

F-THYR01001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058

F-VESEN1000122//HS\_3075\_B1\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749

F-Y79AA1000013

F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//2.9e-95:300:94//AC006027

F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds.//2.4e-19:230:66//L13689



F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521

F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:117:83//Z72005

F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893

F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-165:732:99//AL031864

F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.//9.1e-20:339:65//AC005115

F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//3.7e-72:397:93//AC004854

F-Y79AA1000230

F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232

F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SACP-1) gene, complete cds.//0.0099:547:58//U78522

F-Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.//4.0e-11:424:62//AF035207

F-Y79AA1000313

F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//5.9e-07:173:69//B55085

F-Y79AA1000342//RPCI11-57J6.TK.1 RPCI11 Homo sapiens genomic clone R-57J6, genomic survey sequence.//5.2e-27:151:99//AQ115511

F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987

F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692

F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-21:129:85//AC005484

F-Y79AA1000368//H.sapiens CpG island DNA genomic MseI fragment, clone 12 f1, reverse read cpg12f1.rtlc.//0.00016:53:98//Z56610

F-Y79AA1000405//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL031747

F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061

F-Y79AA1000420//H.sapiens CpG island DNA genomic MseI fragment, clone 82 c3, forward read cpg82c3.ft1a.//2.0e-36:194:98//Z63378

F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds.//8.5e-121:696:89//U41736

F-Y79AA1000480//HS\_2175\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=0, genomic survey sequence.//2.5e-26:178:89//AQ307693

F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.67:111:72//AC004980

F-Y79AA1000539//HS\_2237\_B2\_F10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence.//1.2e-14:168:77//AQ153503

F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.94:127:67//AC005193

F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//1.7e-114:776:84//X14972

F-Y79AA1000574//M.musculus tex23 mRNA (5' region).//1.8e-23:291:75//X80424

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence./

/8.6e-153:755:97//AF091080

F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//5.2e-135:644:98//AF060503

F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//6.9e-148:902:86//X69942

F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds.//4.8e-180:850:98//AB018080

F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5.//0.00019:308:60//U23172

F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein.//1.7e-40:513:68//AJ003023

F-Y79AA1000774

F-Y79AA1000782

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//3.5e-177:847:97//AF098799

F-Y79AA1000794//H.sapiens CpG island DNA genomic MseI fragment, clone 45a4, forward read cpg45a4.ft1a.//2.5e-13:104:92//Z61120

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds.//0.98:244:60//AF056085

F-Y79AA1000802

F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//9.3e-76:528:85//U73642

F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence.//4.4e-14:99:95//B84538

F-Y79AA1000827//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//1.5e-08:249:69//AL022315

F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-103:603:89//X04757

F-Y79AA1000850

F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//0.038:468:59//Z82203

F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.7e-150:865:89//AF071314

F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//6.4e-122:717:88//U38253

F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence.//1.0:155:63//AC002397

F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1.//4.3e-06:130:73//U88165

F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//2.4e-44:428:77//U05823

F-Y79AA1001023

F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds.//2.3e-13:90:100//U63329

F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds.//2.6e-28:772:60//D43682

F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence.//9.4e-36:292:82//AC004701

F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt].//0.17:537:59//S64314

F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds.//0.17:231:64//D88452

F-Y79AA1001078

F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds.//3.1e-63:529:77//D26173

F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.3e-23:228:76//AC005015

F-Y79AA1001167

F-Y79AA1001177//M.musculus mRNA for Nfix1-protein.//4.0e-10:398:64//Y076  
88

F-Y79AA1001185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 169I5, WORKING DRAFT SEQUENCE.//1.1e-113:666:90//Z93015

F-Y79AA1001211//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey  
sequence.//5.5e-12:87:96//AQ187492

F-Y79AA1001216

F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segmen  
t 143/162.//0.028:188:67//AL021841.

F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRN  
A, complete cds.//3.5e-24:731:60//M36263

F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequ  
ence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)  
).//1.2e-133:441:97//AJ005892

F-Y79AA1001281//HS\_2241\_B2\_F09\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey  
sequence.//5.0e-27:169:94//AQ217497

F-Y79AA1001299//Human In11 mRNA, complete cds.//6.7e-115:323:93//U04847

F-Y79AA1001312

F-Y79AA1001323

F-Y79AA1001384

F-Y79AA1001391//Mus musculus transcription factor, HOXA13 (Hoxa13) gene,  
complete cds.//5.8e-42:245:74//U59322

F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence./  
/7.8e-18:636:58//Z48583

F-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer  
Institute Human PAC Library) complete sequence.//1.2e-110:738:85//AC005

924

F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497

F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12  
Contains ESTs and GSSs, complete sequence.//1.1e-158:804:95//AL034430

F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53  
) , complete cds.//1.7e-100:820:78//D14336

F-Y79AA1001541//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey  
sequence.//5.1e-28:218:86//AQ150183

F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequ  
ence.//5.4e-21:167:86//AC004151

F-Y79AA1001555//R.norvegicus mRNA for drebrin A.//0.88:463:59//X59267

F-Y79AA1001581//FMR1 {CGG repeats} [human, Fragile X syndrome patient, G  
enomic, 429 nt] .//0.00051:252:65//S74494

F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene  
, complete cds.//7.2e-33:375:76//M26434

F-Y79AA1001594

F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3,  
containing the HMG-14 and CHD5 genes, complete cds, complete sequence./  
/4.2e-06:338:66//AF064861

F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds.//0  
.024:520:57//AB014583

F-Y79AA1001647//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.014:331:61//Z92860

F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.  
3, complete sequence.//0.99:273:63//Z84468

F-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//1.2e-  
97:682:81//M22743

F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, pla  
centa, Genomic, 1292 nt, segment 1 of 4] .//5.6e-05:426:59//S37712

F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyprotein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60//D32136

F-Y79AA1001705//M.musculus fkh-5 gene.//0.18:153:64//X71943

F-Y79AA1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240

F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE.//0.99:227:63//AP000017

F-Y79AA1001805//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12.rtlc.//2.6e-13:88:100//Z64565

F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//3.7e-130:775:88//U74297

F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence.//8.3e-17:218:76//AQ012369

F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378:62//AB002388

F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKrl) mRNA, complete cds.//6.9e-41:441:71//U41164

F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00017:412:62//AF029779

F-Y79AA1001875//CIT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654

F-Y79AA1001923//H.sapiens CpG island DNA genomic MseI fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186

F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184

F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340

F-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 526I14, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214

F-Y79AA1002089

F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548

F-Y79AA1002103//HS\_3052\_B1\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014

F-Y79AA1002115

F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693

F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358

F-Y79AA1002204//HS\_2235\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260

F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397

F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719

F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615

F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043

F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738

F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045

F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.



3e-174:821:98//AB014592  
 F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 un  
 nordered pieces.//0.50:470:60//AC005015  
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.  
 8e-159:748:98//AB014555  
 F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.  
 //0.036:278:62//U10886  
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.  
 4e-129:622:97//AB014534  
 F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding  
 protein.//2.0e-116:693:82//X67877  
 F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101  
 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-sub  
 unit).//5.4e-105:762:80//Y18208  
 F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete  
 sequence.//1.0e-159:411:100//AC005920  
 F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complet  
 e sequence.//1.1e-118:609:84//AC004662  
 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsh) mRNA, comple  
 te cds.//4.4e-90:529:88//U49385  
 F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, com  
 plete cds.//1.0:166:66//U36196  
 F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K  
 8, genomic survey sequence.//0.24:85:72//B51917  
 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323),  
 complete sequence.//1.9e-13:242:69//AC006116  
 F-Y79AA1002482//Homo sapiens full length insert cDNA clone ZC18H06.//1.2  
 e-35:462:71//AF088022  
 F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//

/0.93:215:60//X94677

【0826】

相同性検索結果データ3.

3'末端クローン配列に対するESTとSTSを除いたGenBank相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのDefinition、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds  
./3.6e-60:504:78//L16953

R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey  
sequence./0.28:117:68//Z88864

R-HEMBA1000042//RPCI11-77G23.TV RPCI11 Homo sapiens genomic clone R-77G2  
3, genomic survey sequence./1.3e-56:292:97//AQ268240

R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence./9.8e-56:401:82//U82696

R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455  
./0.0010:175:68//L31948

R-HEMBA1000076//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6  
unordered pieces./4.9e-41:364:79//AC005520

R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human B  
AC library) complete sequence./4.7e-30:229:84//AC003684

R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete se  
quence./2.4e-93:503:93//AC003104

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds./6.

5e-99:514:94//AB018340

R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:289:83//AC005060

R-nnnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//L43631

R-HEMBA1000158

R-nnnnnnnnnnnnn

R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//X84904

R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.3e-40:286:85//AC006146

R-HEMBA1000193

R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126

R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655

R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:79//AF001548

R-nnnnnnnnnnnnn

R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181

R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:319:69//AC004526

R-HEMBA1000244

R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262

R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr

ome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012

R-nnnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//3.5e-10:238:70//AC003037

R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270

R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:267:82//AC003046

R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//AC004223

R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey sequence.//1.0:215:61//B95105

R-nnnnnnnnnnnnn//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131

R-nnnnnnnnnnnnn//Rattus norvegicus Ca<sup>2+</sup>-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802

R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein.//3.8e-36:315:68//Y10496

R-nnnnnnnnnnnnn//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.078:379:59//AC005505

R-HEMBA1000338//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//2.0e-33:399:72//AL031667

R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//1.7e-39:272:87//AJ003147

R-HEMBA1000355//Human primary Alu transcript.//0.0045:67:85//U67829

R-HEMBA1000357//Homo sapiens (subclone 9\_h8 from P1 H16) DNA sequence.//8.7e-93:426:88//L42086

R-HEMBA1000366//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-12:130:83//AC006012

R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//1.9e-69:355:97//AL031587

R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//3.7e-66:410:89//AC006116

R-HEMBA1000387//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:363:81//AC002993

R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//4.6e-23:417:69//AC005053

R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//AC004582

R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575

R-HEMBA1000411

R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.94:210:60//X04465

R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey sequence.//4.4e-12:98:92//AQ078233

R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//2.0e-93:526:90//Z95400

R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-07:452:60//AC004826

R-HEMBA1000442//E.caballus microsatellite DNA, clone HMB4.//0.39:135:62//Y07733

R-HEMBA1000456//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*

from contig 4-52, complete sequence.//2.6e-05:174:70//AL010226

R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein Glp (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (AT EM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, complete cds; and unknown genes.//0.013:212:63//AF049236

R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//8.6e-114:556:98//AC004839

R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence.//0.086:334:61//Z83220

R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.8e-52:472:79//AC005104

R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500

R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence.//0.97:233:61//Z99278

R-HEMBA1000491

R-HEMBA1000504//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete sequence.//1.7e-08:440:60//AL009014

R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11.//0.37:189:62//AB020858

R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//1.1e-25:248:80//Z70280

R-HEMBA1000518//RPCI11-6022.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6022, genomic survey sequence.//0.0035:293:61//B49544

R-HEMBA1000519

R-HEMBA1000520//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.30:255:63//AC006232

R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782

R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388 J17, genomic survey sequence.//2.7e-24:137:99//B55638

R-HEMBA1000540//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103

R-nnnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555

R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381

R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762

R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368

R-HEMBA1000568//RPCI11-49P8.TK.1 RPCI11 Homo sapiens genomic clone R-49P8, genomic survey sequence.//1.7e-101:498:97//AQ116293

R-nnnnnnnnnnnnn

R-HEMBA1000575//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335

R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:94//AJ007509

R-HEMBA1000592//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216

R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-15:421:66//AC005044

R-HEMBA1000604//HS\_2220\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991

R-HEMBA1000608

R-HEMBA1000622//H.sapiens CpG island DNA genomic MseI fragment, clone 155e4, reverse read cpg155e4.rtl1a.//4.5e-16:105:98//Z56962

R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008

R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:97//AB014590

R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953

R-HEMBA1000657

R-HEMBA1000662

R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196

R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-50:298:79//AC005377

R-HEMBA1000686//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513

R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.7e-54:317:88//AC005000

R-HEMBA1000705//Glossonotus univittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77850

R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:58//D50864



R-HEMBA1000722

R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q36, complete sequence.//4.4e-26:284:77//AC005531

R-HEMBA1000727//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266

R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6 q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.5e-16:123:93//AL021326

R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327024, complete sequence.//2.8e-32:298:79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545

R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-36:405:75//AC005031

R-HEMBA1000773//HS\_3050\_A2\_B08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619

R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000791//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571

R-HEMBA1000817//Sequence 1 from Patent WO 8904839.//0.86:148:67//I09339

R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA.//0.00061:246:61//Z15118

R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM 160) mRNA, complete cds.//6.9e-43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome

e 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSS and GSSs, complete sequence.//1.7e-41:319:84//AL022394

R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180 G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC002042

R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057

R-HEMBA1000908//CIT-HSP-2373I4.TR CIT-HSP Homo sapiens genomic clone 2373I4, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

R-HEMBA1000918//RPCI11-68E14.TK RPCI11 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224

R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 C contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311

R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888

R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.7e-37:296:83//AC005632

R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 Homo sapiens genomic clone RPCI

-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952  
R-HEMBA1001007  
R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365  
R-HEMBA1001009//O.sativa osr40g2 gene.//0.99:203:62//Y08987  
R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937  
R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547  
R-HEMBA1001020//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722  
R-HEMBA1001022  
R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//6.6e-48:536:74//AF070717  
R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363  
R-nnnnnnnnnnnnn//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686  
R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217  
R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751  
R-HEMBA1001060//HS\_2056\_B1\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004  
R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-I.//6.9e-38:513:70//X52046  
R-HEMBA1001077//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318  
R-HEMBA1001080  
R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing  
fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 un-  
ordered pieces.//2.2e-43:317:83//AC004586  
R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067  
607  
R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98  
:501:96//AC005105  
R-HEMBA1001099  
R-HEMBA1001109//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527  
R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8  
e-11:122:81//U81833  
R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024  
:284:63//Z98551  
R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511  
R-HEMBA1001133  
R-HEMBA1001137//Homo sapiens full length insert cDNA clone ZD29F04.//4.2  
e-88:426:98//AF086241  
R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 u-  
nordered pieces.//4.0e-41:304:84//AC005077  
R-HEMBA1001172//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304  
R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of  
the complete sequence.//1.0:219:58//AE001398  
R-HEMBA1001197  
R-HEMBA1001208//HS\_2233\_A1\_G10\_MF CIT Approved Human Genomic Sperm Libra-  
ry D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey

sequence.//0.083:174:68//AQ170789

R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377

R-HEMBA1001235//RPCI11-50E6.TJ RPCI11 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052666

R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1.//2.4e-05:319:63//U58761

R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.//1.5e-24:439:66//U89905

R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//9.9e-21:537:63//AC004491

R-nnnnnnnnnnnnn//Homo sapiens chromosome 17, clone HCIT75G16, complete sequence.//0.022:169:65//AC003042

R-HEMBA1001286

R-HEMBA1001289

R-HEMBA1001294//HS\_3219\_A2\_G01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882

R-HEMBA1001299//Homo sapiens, clone hRPK.12\_A\_1, complete sequence.//1.3e-38:381:76//AC006222

R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258

R-HEMBA1001303//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744

R-HEMBA1001310

R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504

R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:4

85:60//X03240

R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6 . Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//2.2e-14:277:69//AL021368

R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.15:360:61//AL024509

R-HEMBA1001330//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216

R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//7.1e-45:252:94//AC006238

R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//1.4e-113:569:97//AC006241

R-HEMBA1001375//Homo sapiens full length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542

R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865

R-HEMBA1001383

R-HEMBA1001387

R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//8.9e-06:108:83//AC005073

R-HEMBA1001391//Yeast mitochondrial aap1 gene for ATPase subunit 8.//7.3e-08:500:59//X00960

R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21

/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050  
R-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 50024, WORKING DRAFT SEQUENCE.//5.5e-35:464:68//AL034380  
R-HEMBA1001407  
R-HEMBA1001411//Yeast (*S.cerevisiae*) mitochondria Ser-tRNA-UCN gene and  
flanks.//0.00029:301:62//K01981  
R-HEMBA1001413  
R-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 41018, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732  
R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//6.3e-37:302:81//AC006146  
R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome Xp11.2.  
Contains KIAA0178 gene, similar to mitosis-specific chromosome segregat  
ion protein SMC1 of *S.cerevisiae*, DNA binding protein similar to URE-B1,  
ESTs and STS.//1.9e-32:242:79//Z97054  
R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) re  
lated locus, complete sequence.//5.7e-59:457:82//AC004527  
R-HEMBA1001442//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-  
27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STS  
s and a polymorphic CA repeat.//0.051:276:63//Z98950  
R-HEMBA1001446//HS\_3207\_A1\_A08\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey  
sequence.//8.9e-06:119:73//AQ175385  
R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete se  
quence.//0.0043:266:63//AC005065  
R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete seq  
uence.//7.1e-25:210:82//AC004855  
R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complet  
e sequence.//2.7e-08:316:62//AC005324



R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence.//0.57:219:60//AC005208

R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//9.3e-50:252:80//AC004840

R-HEMBA1001478

R-HEMBA1001497

R-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337

R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. C contains EST and STS.//1.9e-79:529:86//Z98753

R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549

R-HEMBA1001522

R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//5.6e-08:265:67//Z98258

R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1. Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053

R-HEMBA1001557

R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383

R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77040

R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453

R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//A

C005506

R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276

R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6.//0.68:224:62//U4101  
2

R-HEMBA1001589

R-HEMBA1001595//CIT-HSP-2349G19.TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence.//8.0e-69:337:99//AQ060483

R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177

R-HEMBA1001620//S.polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693

R-nnnnnnnnnnnnn//HS\_2195\_A1\_E09\_MF CIT Approved Human Genomic Spermlibrary D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence.//5.8e-09:358:58//AQ292688

R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270

R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS.//6.0e-49:404:79//Z84484

R-nnnnnnnnnnnnn

R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368

R-HEMBA1001658//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808

R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740

R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247

R-HEMBA1001675

R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds.//1.3e-101:534:94//AF038962

R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593

R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801

R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds.//1.9e-96:483:96//AB014598

R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886

R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65//B32577

R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250

R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781

R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//0.53:275:61//AF018261

R-HEMBA1001731//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799

R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959

R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067

R-HEMBA1001745//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete

sequence.//0.00019:312:59//AC005084

R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153

R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//3.8e-39:331:80//AC006121

R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554

R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740

R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575

R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222

R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC005506

R-nnnnnnnnnnnnn//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//2.9e-93:553:89//M21977

R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//2.8e-112:548:98//AB007969

R-HEMBA1001809

R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//2.6e-48:363:84//AC004025

R-HEMBA1001819//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612

R-HEMBA1001820//HS\_3022\_B1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey

sequence.//0.00054:335:59//AQ165107

R-nnnnnnnnnnnnn//Xenopus laevis intersectin mRNA, complete cds.//1.4e-19:533:63//AF032118

R-HEMBA1001824//S.clavuligerus linear plasmid pSCL (complete sequence).//0.62:189:65//X54107

R-HEMBA1001835//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507

R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds.//1.6e-07:170:68//U50871

R-HEMBA1001847

R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3.3e-108:553:96//AB014517

R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001866//HS\_2258\_B2\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence.//2.8e-39:397:75//AQ221138

R-nnnnnnnnnnnnn//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//5.9e-56:303:94//AC005065

R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.7e-43:281:88//AC006210

R-HEMBA1001896

R-HEMBA1001910

R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.10:307:61//AC004775

R-HEMBA1001913

R-HEMBA1001915//HS\_2037\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence.//0.071:206:64//AQ233106

R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.97:449:59//AC004775

R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.0e-105:534:96//AF000145

R-HEMBA1001939//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//4.6e-13:120:82//AL021707

R-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-36:301:81//AC005629

R-HEMBA1001942//Human PAC clone DJ0205E24 from Xq23, complete sequence.//1.9e-10:208:68//AC003013

R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//1.2e-06:393:60//AE001433

R-HEMBA1001950//R.prowazekii genomic DNA fragment (clone A437R).//0.33:122:66//Z82646

R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) gene, complete cds.//0.0086:427:59//U05329

R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//4.5e-07:176:70//AC004069

R-HEMBA1001964//HS\_2215\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey sequence.//7.3e-25:215:74//AQ151931

R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive iso log of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//1.7e-51:209:95//AL031178

R-HEMBA1001979//CIT-HSP-2387I12.TF.1 CIT-HSP Homo sapiens genomic clone 2387I12, genomic survey sequence.//4.9e-06:153:71//AQ240461

R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3

-23. Contains an EST, an STS and GSSs, complete sequence.//3.1e-46:437:77//AL033521

R-HEMBA1001991//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-48:446:78//AL020997

R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta).//5.1e-90:448:97//AJ005801

R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.2e-42:317:84//Z97181

R-HEMBA1002018//HS\_3006\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H, genomic survey sequence.//1.0:63:74//AQ089717

R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453\_M\_1, complete sequence.//0.93:339:59//AC006203

R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694

R-HEMBA1002039

R-HEMBA1002049//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315

R-HEMBA1002084//CIT-HSP-2357L11.TR CIT-HSP Homo sapiens genomic clone 2357L11, genomic survey sequence.//0.0013:185:66//AQ063078

R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703

R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357

R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800

R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence.//1.6

e-64:550:80//U47924

R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1  
.2e-92:435:92//AC000378

R-HEMBA1002125

R-HEMBA1002139//Human nebulin mRNA, partial cds.//0.056:68:88//U35637

R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 contain  
ing tryptophan hydroxylase gene, complete sequence.//2.0e-26:323:70//AC  
005728

R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12  
.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide  
de VB and (parts of) up to four novel genes, two with homology to Phorbol  
lin genes and one a novel Chromobox protein gene. Contains ESTs, an STS,  
GSSs and putative CpG islands, complete sequence.//1.0:371:61//AL031846

R-HEMBA1002151

R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence.//  
/2.4e-21:322:70//AC003971

R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2.  
Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation  
protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1,  
ESTs and STS.//2.5e-38:216:84//Z97054

R-HEMBA1002161//CIT-HSP-2163F10.TF CIT-HSP Homo sapiens genomic clone 21  
63F10, genomic survey sequence.//3.1e-58:284:80//B89969

R-HEMBA1002162//Caenorhabditis elegans cosmid F48C11, complete sequence.  
//0.0079:286:57//Z80789

R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library  
) complete sequence.//5.9e-53:326:80//AC002980

R-HEMBA1002177

R-HEMBA1002185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 745I14, WORKING DRAFT SEQUENCE.//9.5e-37:356:76//AL033532



R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.4e-43:244:77//AC003684

R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.3e-37:323:78//AC005077

R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.3, complete sequence.//1.4e-89:564:87//AC002498

R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGL C Region, complete sequence.//1.5e-31:313:71//AC000053

R-HEMBA1002212//K.lactis mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase subunit 8.//0.0023:346:60//X57546

R-HEMBA1002215//M.musculus mRNA for testin.//4.7e-61:414:84//X78989

R-HEMBA1002226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.//4.6e-46:375:77//AL033529

R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.6e-46:238:98//AF089814

R-HEMBA1002237//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.3e-26:469:67//AC004242

R-HEMBA1002253//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//5.1e-23:162:82//AC005016

R-HEMBA1002257

R-HEMBA1002267//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//4.6e-44:300:88//AF038127

R-HEMBA1002270//Human BAC clone RG067M09 from 7q21-7q22, complete sequence.//1.9e-19:176:85//AC000057

R-HEMBA1002321

R-HEMBA1002328//HS\_3061\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=11 Row=G, genomic survey sequence.//1.0:151:65//AQ127617

R-HEMBA1002337//Saccharomyces cerevisiae RNA polymerase II holoenzyme component (SRB7) gene, complete cds.//3.7e-07:328:63//U23811

R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-128:642:96//AB018314

R-HEMBA1002348//Human DNA sequence from clone 409010 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//3.7e-07:587:58//AL031256

R-HEMBA1002349//Leishmania tarentolae maxicircle DNA fragment.//0.018:341:58//X02438

R-nnnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//1.2e-121:661:93//AF092563

R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 11/11 .//1.1e-70:559:79//AB020868

R-HEMBA1002389//HS\_3218\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=J, genomic survey sequence.//0.0011:122:72//AQ213602

R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//4.2e-81:232:97//AC005954

R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.50:231:64//AC004848

R-HEMBA1002430//P.falciparum complete gene map of plastid-like DNA (IR-B ).//0.0023:604:56//X95276

R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-23:183:80//AC006026

R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYT OCHROME B-245 HEAVY CHAIN. pseudogene similar to hnRNP A1 protein and ESTs, complete sequence.//7.7e-32:161:83//Z83819

R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//2.6e-100:305:100//AC005378

R-HEMBA1002462//Sequence 43 from patent US 5708157.//2.0e-10:131:77//I80068

R-nnnnnnnnnnnnnnn

R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.//6.6e-33:279:80//AC004841

R-HEMBA1002486//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//2.1e-50:290:92//U14573

R-HEMBA1002495//CITBI-E1-2515J10.TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey sequence.//1.0:122:68//AQ261762

R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//2.8e-22:210:78//AC004963

R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//2.7e-17:435:58//AC003043

R-HEMBA1002508//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.7e-09:408:61//AC006213

R-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//7.1e-112:456:92//AJ011972

R-HEMBA1002515

R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds.//1.6e-104:564:93//AB007923

R-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//2.8e-25:186:86//AQ188792

R-HEMBA1002547//Mus musculus agrin gene, exon 36.//0.0095:93:75//M92658

R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-49:308:90//AC005378

R-HEMBA1002555//Homo sapiens full length insert cDNA clone YR87G10.//8.3

e-65:318:99//AF085957

R-HEMBA1002558//, complete sequence.//2.3e-38:264:89//AC005409

R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.1e-44:192:80//AL008634

R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//4.5e-119:587:97//AF075587

R-HEMBA1002583

R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-42:248:88//Z95152

R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//2.6e-56:302:84//AC004510

R-HEMBA1002621

R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//6.7e-76:380:97//AB018351

R-HEMBA1002628//P.falciparum complete gene map of plastid-like DNA (IR-A).//8.8e-05:327:60//X95275

R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence.//4.3e-06:205:66//AF046247

R-HEMBA1002645//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.1e-39:281:84//U14567

R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//1.1e-104:500:95//AC004839

R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.2e-61:280:92//AL022323

R-HEMBA1002661//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 225E12, WORKING DRAFT SEQUENCE.//3.2e-41:325:81//AL031772

R-HEMBA1002666//Homo sapiens full length insert cDNA clone YY74A07.//0.0  
 0037:79:84//AF088008

R-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 1137F22, WORKING DRAFT SEQUENCE.//2.3e-107:561:94//AL034421

R-nnnnnnnnnnnnn//CIT-HSP-2287E8.TF CIT-HSP Homo sapiens genomic clone 228  
 7E8, genomic survey sequence.//5.4e-17:137:88//B99281

R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), c  
 omplete sequence.//0.033:146:70//AC004503

R-HEMBA1002696

R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence  
 .//6.2e-44:302:87//AC003982

R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds.//1.1e-31:332:7  
 6//AB004873

R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds.//1.  
 2e-35:287:81//AB014521

R-HEMBA1002730//D.discoideum actin M6 gene, 5' flank.//0.018:233:66//M29  
 109

R-HEMBA1002742//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 1108H3, WORKING DRAFT SEQUENCE.//2.6e-13:419:62//AL033525

R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete se  
 quence.//0.019:202:65//AC003694

R-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
 lone 404K8, WORKING DRAFT SEQUENCE.//0.046:263:60//AL023883

R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X conta  
 ins sodium-and chloride-dependent glycine transporter 1 (GLYT-1) like, E  
 STs.//0.052:421:58//Z96810

R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//1.

2e-104:545:95//AB011126

R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.0e-07:523:59//AC005140

R-HEMBA1002777

R-HEMBA1002779//Human HepG2 3' region MboI cDNA, clone hmd1e03m3.//9.4e-25:158:93//D17139

R-HEMBA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.6e-42:463:75//AL022344

R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence.//2.2e-05:417:59//AL034560

R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.//0.00055:444:59//L76261

R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//4.4e-115:559:97//AF071185

R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.3e-88:329:94//AC005043

R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//1.9e-22:262:67//AP000041

R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.3e-79:396:97//AC004707

R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.013:393:61//AC005506

R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//4.1e-73:489:85//AC005562

R-HEMBA1002876//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.21:549:55//AL034557

R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey sequence.//0.30:431:56//B53836

R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds.//3.9e-106:541:95//AF037261

R-HEMBA1002921

R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10.//4.6e-19:139:78//AB020875

R-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//7.5e-45:282:89//AL031681

R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey sequence.//1.5e-102:514:97//AQ008584

R-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745I14, WORKING DRAFT SEQUENCE.//3.3e-87:444:97//AL033532

R-HEMBA1002939

R-HEMBA1002944//HS\_3107\_A1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=9 Row=E, genomic survey sequence.//6.3e-21:250:73//AQ103952

R-HEMBA1002951//Xerolycosa miniata mitochondrial 12S rRNA gene.//0.013:228:63//AJ008020

R-HEMBA1002954//HS\_3246\_A2\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005

R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//4.2e-38:300:83//AC005553

R-HEMBA1002970//Slime mold (D.discoideum) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012

R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579

R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequ

ence.//9.1e-36:520:69//AC006128  
R-nnnnnnnnnnnnn//Homo Sapiens Chromosome X clone bWXd691, complete sequence.//0.00040:504:59//AC004386  
R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1 C) mRNA, complete cds.//3.7e-66:556:79//U19614  
R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406  
R-HEMBA1003033//Homo sapiens full length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194  
R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026  
R-HEMBA1003035//HS\_2008\_A2\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839  
R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694  
R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983  
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182  
R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962  
R-HEMBA1003067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302  
R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136  
R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975



R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2.

Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of *S.cerevisiae*, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054

R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673

R-HEMBA1003083//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798

R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-43:281:88//AC006039

R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213

R-HEMBA1003098//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598

R-HEMBA1003117

R-HEMBA1003129//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329

R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-99:484:98//AC004472

R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861

R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024

R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-116:586:96//AJ005670

R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X contain

ns ESTs.//6.4e-35:364:70//Z83822

R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor.//1.9e-30:282:77//X60459

R-HEMBA1003197

R-HEMBA1003199//HS\_2166\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=23 Row=I, genomic survey sequence.//0.00026:271:61//AQ164162

R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.4e-44:291:83//AC005480

R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//3.1e-10:293:62//AC000118

R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.0:118:69//AC006148

R-HEMBA1003220//HS\_3092\_B1\_F09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=17 Row=L, genomic survey sequence.//0.00014:59:91//AQ128202

R-HEMBA1003222//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y43F8, WORKING DRAFT SEQUENCE.//0.84:214:62//Z95393

R-HEMBA1003229//RPCI11-16F15.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16F15, genomic survey sequence.//0.42:167:64//B83610

R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey sequence.//3.6e-36:195:81//AQ037231

R-HEMBA1003250//HS\_2168\_A2\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=18 Row=E, genomic survey sequence.//1.4e-22:158:89//AQ125356

R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:268:61//U53709

R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//1.0e-32:255:84//AC002549

R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0044:212:60//AC005308

R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-34:286:74//AC002395

R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.8e-53:428:83//AC005840

R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//3.0e-115:551:99//AB011109

R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey sequence.//2.9e-20:337:65//AQ003073

R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:97//I25662

R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence.//0.00019:334:60//AB017061

R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//2.8e-111:545:97//AB001872

R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.60:274:61//AL022153

R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.//0.00028:172:65//AC005099

R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.2e-44:268:90//AC005081

R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds.//2.7e-61:312:97//AF026029

R-HEMBA1003348//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.2e-38:186:83//U14567

R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence./

/0.00012:465:59//Z79600

R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.//3.2e-42:301:87//AC002558

R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21. 2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF 127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.4e-34:375:74//AL022721

R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//1.6e-46:309:88//AC004651

R-HEMBA1003380//HS\_3184\_B2\_E06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=12 Row=J, genomic survey sequence.//1.0e-35:237:88//AQ189144

R-HEMBA1003384//HS\_2193\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, genomic survey sequence.//0.00029:96:76//AQ032212

R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.6e-21:139:86//AC002993

R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic clone 2166E19, genomic survey sequence.//0.99:144:61//B91549

R-nnnnnnnnnnnnnnn

R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11. 2-12.3 Contains EST, GSS, complete sequence.//2.5e-112:547:98//AL031321

R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//0.082:352:59//AC004879

R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NBS1) mRNA, complete cds.//9.9e-114:544:98//AF058696

R-HEMBA1003461  
R-HEMBA1003463  
R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//9.1e-106:533:96//AC005041  
R-HEMBA1003528  
R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//3.4e-08:333:64//AC002454  
R-HEMBA1003538//Human mRNA for complement component C1r.//1.4e-23:333:68//X04701  
R-HEMBA1003545//Zebrafish mRNA for zflsl-2 (insulin gene enhancer binding protein homolog), complete cds.//0.030:144:68//D38453  
R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0017:487:57//AC004153  
R-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//2.8e-99:503:96//AL031718  
R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//1.6e-114:574:97//AC005913  
R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096.//0.24:116:67//AF034416  
R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.9e-05:422:63//AC006036  
R-HEMBA1003569//Homo sapiens full length insert cDNA clone ZD82D06.//8.7e-108:545:95//AF086450  
R-HEMBA1003571//Homo sapiens PAC clone DJ0886008 from 7q32-q35, complete sequence.//4.6e-51:570:71//AC004914  
R-HEMBA1003579//HS\_3237\_B2\_E05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, genomic survey sequence.//8.5e-97:495:95//AQ209302

R-HEMBA1003581//Mouse mRNA for talin.//8.3e-12:128:82//X56123

R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL), complete sequence.//2.9e-87:251:95//AC005774

R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//4.5e-52:384:83//AL008715

R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSS, complete sequence.//4.6e-41:442:74//Z84480

R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.8e-23:177:88//AC005153

R-HEMBA1003615

R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:494:57//AC005139

R-HEMBA1003621//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.3e-26:309:75//AC004599

R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//7.1e-56:545:75//AC002980

R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete sequence.//2.8e-32:546:68//AF088219

R-HEMBA1003637//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//8.0e-25:457:68//AC002454

R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete sequence.//2.8e-40:280:86//AF031078

R-HEMBA1003645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//1.7e-33:297:82//AL023693

R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence.//0.44:319:59//AL034559

R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-36:242:80//AC004382

R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.6e-117:588:96//AC005746

R-HEMBA1003667//Sequence 8 from patent US 5420245.//1.8e-21:170:88//I12222

R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.6e-22:180:87//AC005065

R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06:270:61//L15313

R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.77:171:66//AF044872

R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-104:523:97//AC004466

R-HEMBA1003692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.7e-41:414:77//AL021707

R-HEMBA1003711//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-29:304:77//AC000406

R-HEMBA1003714

R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-685D8, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-63:578:77//AC005136

R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered piec

es.//2.4e-36:350:78//AC002353

R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//6.3e-42:250:75//AC004699

R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22D14, genomic survey sequence.//1.0:234:62//B86158

R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.7e-80:558:83//AL008634

R-HEMBA1003742//HS\_3080\_B2\_H06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence.//3.4e-55:331:91//AQ139179

R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and CpG island.//4.5e-59:521:75//Z97876

R-HEMBA1003760

R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//2.6e-72:467:86//U17343

R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.0e-77:557:81//AF084259

R-HEMBA1003784

R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence.//2.1e-49:390:72//AC004455

R-HEMBA1003803

R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//9.4e-99:359:99//AC004596

R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.0e-113:567:96//AL031781



R-HEMBA1003807//Bovine dinucleotide microsatellite HUJ1177.//5.4e-18:194:78//M96348

R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//3.4e-40:256:85//AC002115

R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence.//9.7e-25:150:96//AQ196624

R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSS, GSSs and a CA repeat polymorphism, complete sequence.//4.8e-33:486:68//Z93929

R-HEMBA1003864//, complete sequence.//4.4e-100:531:94//AC005300

R-HEMBA1003866//HS\_3203\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298

R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207

R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036

R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576

R-HEMBA1003893//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421

R-HEMBA1003902//HS\_3031\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549

R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795

R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158),

complete sequence.//3.1e-58:294:85//AC005368  
R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111  
:590:93//AF109718  
R-HEMBA1003939  
R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-0  
8:474:58//AC004904  
R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, m  
itochondrial gene encoding mitochondrial protein, partial cds.//0.034:25  
8:62//AF069619  
R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:  
492:57//AL034560  
R-HEMBA1003958//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668  
R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenas  
e (ahybadh4) gene, complete cds.//0.11:428:60//AF000132  
R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, comple  
te sequence.//1.0:222:62//AC004414  
R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//I80  
060  
R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Canc  
er Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC00  
4804  
R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2  
e-26:268:79//U47924  
R-HEMBA1003989//RPCI11-52K22.TJ RPCI11 Homo sapiens genomic clone R-52K2  
2, genomic survey sequence.//2.2e-86:443:95//AQ052484  
R-HEMBA1004000  
R-HEMBA1004011  
R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete